

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:57:42 : Search time 4967 seconds

(without alignments)

13384.835 Million cell updates/sec

Title: US-09-931-157-1

Perfect score: 4105

Sequence: 1 gaattcggcgccgtcttg.....taaaagttacagaacatt 4105

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

sarched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	797.8	19.4	865	9	AU118882	AU118882	AU118882
2	792.2	19.3	863	9	AU119546	AU119546	AU119546
3	789	19.2	869	9	AU120519	AU120519	AU120519
c 4	725.6	17.7	781	9	A1936539	wd29b09.x	A1936539
5	710.4	17.3	733	14	BM719244	BM719244	BM719244
c 6	704.2	17.2	777	14	BQ018994	BQ018994	BQ018994

RESULT 1

AU118882

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AU118882

AU118882

sequence.

AU118882

AU118882.1

GI:10934117

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria;

1 (bases 1 to 865)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

Unpublished (2000)

Contact: Takao Isogai

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Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project: 5' - & 3' - end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

ALIGNMENTS

865 bp mRNA linear EST 01-AUG-2002
Homo sapiens cDNA clone HEMBA1004569 5', mRNA

AU139639 AU139639
AI694278 wd45a01.x
BQ575745 UI-H-E21-
AI809396 wf70b01.x
BQ006584 UI-H-E11-
BG116534 602317635
BG699589 602679314
AI130721 qcl6el2.x
AI1953824 wx69h09.x
BM548868 AGENCOURT
AU117099 AU117099
AK017486 Mus muscu
AI1913052 tz75f01.x
AI804414 tc71a03.x
BF984079 602307535
BM998050 UI-H-DT1-
BG114663 602315469
BM683196 UI-E-E01-
BF980903 602304437
AI417092 tg78905.x
BM512298 ij70c02.x
BE813325 RC3-BN003
BE328379 hs93q06.x
BG548379 602575155
AI144480 qb72e08.x
AI240165 qb39f10.x
AU234178 zr49f02.r
AU145859 AU145859
AL692187 DKF7P313C
AU145342 AU145342
AA52627 zx33f03.r
AI252673 qh86c11.x
AA910453 oj89h09.s
AI332625 qg28b02.x
AU158110 AU158110
AA058926 z196f11.r
AA406195 zv24d09.s
AU116816 AU116816
AI475501 tj92h05.x

764 9 AU139639
739 9 AI694278
732 14 BQ575745
747 9 AI809396
705 14 BQ006584
742 12 BG116534
771 12 BG699589
677 9 AI130721
724 9 AI1953824
1072 13 BM548868
708 9 AU117099
1627 11 AK017486
700 9 AI1913052
678 9 AI804414
652 12 BF984079
637 14 BM998050
1043 12 BG114663
621 14 BM683196
918 12 BF980903
674 9 AI417092
595 13 BM512298
645 12 BE813325
609 10 BE328379
676 12 BG548379
582 9 AI144480
572 9 AI240165
595 9 AA234178
560 9 AU145859
553 9 AL692187
597 9 AU145342
580 9 AA52627
554 9 AI252673
660 9 AA910453
524 9 AI332625
552 9 AU158110
599 9 AA058926
563 9 AA406195
664 9 AU116816
549 9 AI475501

695.8 17.0
634.4 16.9
652.2 16.9
687.8 16.8
685 16.7
705 16.6
683 16.6
673 16.4
653.4 15.9
650.6 15.8
649.8 15.8
640.8 15.6
627 15.3
621.6 15.1
611 14.9
610 14.9
603.2 14.7
603 14.7
596.8 14.5
595.4 14.5
595 14.5
582.2 14.2
569 13.9
563.2 13.7
561.8 13.7
552.6 13.5
534.8 13.0
534.4 13.0
525.8 12.8
524.8 12.8
521 12.7
520.4 12.7
519.6 12.7
516.4 12.6
514.4 12.5
513.8 12.5
513.2 12.5
512.4 12.5
512.2 12.5

FEATURES	source	Location/Qualifiers
Db	841	CNCNTAGTTTGAAAAAAGGAC 864
RESULT 2		
AU119546		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
FEATURES		
Source		
BASE COUNT	285 a	130 c 130 g 316 t 2 others
ORIGIN		
Query Match	19.3%	Score 792.2; DB 9; Length 863;
Best Local Similarity	97.8%	Pred. No. 8.5e-168;
Matches	845; Conservative	0; Mismatches 14; Indels 5; Gaps 4;
QY	2045	GAACACAGAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAGTACATGCTAG 2104
Db	1	GAACACAGAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAGTACATGCTAG 60
QY	2105	CTTTTATGCGAGTCTGCTGGAATGTTCAATGGAACTGCTCACCATGAACTTTAGAGAT 2164
Db	61	CTTTTATGCGAGTCTGCTGGAATGTTCAATGGAACTGCTCACCATGAACTTTAGAGAT 120
QY	2165	TAACGACAGAGATTTTCTACTTTTAAAGTGA- -TTTTTTGTCCCTTCAGCCAAACACAA 2222
Db	121	TAACGACAGAGATTTTCTACTTTTAAAGTGAATTTTGTCTTCAGCCAAACACAA 180
QY	2223	ATGGGCTCAGGTCACCTTTTAAAGTGAATTTTGGTGGCCAGTATTTTAACTGCATA 2282
Db	181	ATGGGCTCAGGTCACCTTTTAAAGTGAATTTTGGTGGCCAGTATTTTAACTGCATA 240
QY	2283	ATAGGCTAACATGATTTTAAAGTGAATTTTACACATAGTTTCAAAAAAAGACAA 2342
Db	241	ATAGGCTAACATGATTTTAAAGTGAATTTTAACTATTTTACACATAGTTTCAAAAAAAGACAA 299
QY	2343	TAGTATTCAGGTGACCAATTTAGATTTTCCACGCTCAGTATTTTAACTATTTTAACT 2402
Db	300	TAGTATTCAGGTGACCAATTTAGATTTTCCACGCTCAGTATTTTAACTATTTTAACT 359


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DEFINITION wd29b09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2329529 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI936539
VERSION AI936539.1 GI:5675409
KEYWORDS EST...
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1132 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
FEATURES
     source
     1..781
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:2329529"
        /clone_lib="Soares_NFL_T_GBC_S1"
        /lab_host="DH10B"
        /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
        a modified polylinker; Site.1: Not I; Site.2: Eco RI;
        Equal amounts of plasmid DNA from three normalized
        libraries (fetal lung NBHL19W, testis NHT, and B-cell
        NCI CGAP GCBI) were mixed, and ss circles were made in
        vitro. Following HAP purification, this DNA was used as
        tracer in a subtractive hybridization reaction. The driver
        was PCR-amplified cDNAs from pools of 5,000 clones made
        from the same 3 libraries. The pools consisted of
        I.M.A.G.E. clones 297480-302087, 682632-687239,
        726408-728711, and 729096-731399. Subtraction by Bento
        Soares and M. Fatima Bonaldo.
        264 a 154 c 129 g 232 t 2 others
BASE COUNT 264 a 154 c 129 g 232 t 2 others
ORIGIN
Query Match 17.7%; Score 725.6; DB 9; Length 781;
Best Local Similarity 97.1%; Pred. No. 8.8e-153;
Matches 748; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 3336 CAACCTGCCCTCAGTCCATTTTAACTCTGTAGCAACCTTCTGCATTATCAATAATCTGTGAATC 3395
|||||
773 CAAACAGCTTCAGTCCATTTT-ACCTGTAGCAACCGTCTGCATTATCAATAATCTGTAGTC 715

QY 3396 ATGTTACCATCAAAATGGATATAAGCAGCGAGCGTGAACGACGATGAGCTGTGGACTAG 3455
|||||
714 ATGTACCATCAATACNAATGGATATAAGCAGCGTGAACGACGATGAGCTGTGGACTAAG 655

QY 3456 CAATATAGGTTTGTGTTGGTGTGCTGTGATGAAGCAGCTATTTGGGGTCATATGCTT 3515
|||||
654 CAATATAGGTTTGTGTTGGTGTGTTGATANAGCAGTATTTGGGGTCATATGCTT 595

QY 3516 TCCTGTCTGGAGCAAAAGTCATTACACTTTGAAGTATATATGTTCTTATCTCAATT 3575
|||||
594 TCCTGTCTGGAGCAAAAGTCATTACACTTTGGAGTATATATGTTCTTATCTCAATT 535

QY 3576 CAATGTGGTGATGAAATGCGAGGTTGCTGTGATATTTCTTTCAGACTTCGCCAGACAGAT 3635
|||||
534 CAATGTGGTGATGAAATGCGAGGTTGCTGTGATATTTCTTTCAGACTTCGCCAGACAGAT 475

QY 3636 TCGTGATAAATAATAGGTAAAGTAATAATTTGTTGGGCCATATTTTAGACAGGTAATAATA 3695
|||||
474 TCGTGATAAATAATAGGTAAAGTAATAATTTGTTGGGCCATATTTTAGACAGGTAATAATA 415

QY 3696 CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAGTACTGCCCTTTTGTGTGTAGC 3755
|||||

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Db 414 CATCAGGTTCCAGTTCGTTGAATTGCAAGGCTAAGAGTACTGCCCTTTTGTGTGTAGC 355
|||||
QY 3756 AGTCAAAATCTATTATTCCTACTGCGCGCATCATATGCAAGTATATGCTATATATAAAGC 3815
|||||
Db 354 AGTCAAAATCTATTATTCCTACTGCGCGCATCATATGCAAGTATATGCTATATATAAAGC 295
|||||
QY 3816 CATAGTTTCACACCAATTTGTTTAGACAATTTGCTTTTTCAGATGCTTTGTTCTTTT 3875
|||||
Db 294 CATAGTTTCACACCAATTTGTTTAGACAATTTGCTTTTTCAGATGCTTTGTTCTTTT 235
|||||
QY 3876 CATATGAAAAAATGCAATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACG 3935
|||||
Db 234 CATATGAAAAAATGCAATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACG 175
|||||
QY 3936 TGCATTTTATTTATGGACGCTGGAAGTAACTGTTTACTAGCAGGAATATTTCCAAATTT 3995
|||||
Db 174 TGCATTTTATTTATGGACTGGTAACTGTTTACTAGCAGGAATATTTCCAAATTT 115
|||||
QY 3996 CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCAGAGCCAAAGGCC 4055
|||||
Db 114 CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCAGAGCCAAAGGCC 55
|||||
QY 4056 CTGAGTTGGCAGTGGCCCATAGTGTAAATAAAGTTTACAGAAACCTT 4105
|||||
Db 54 CTGAGTTGGCAGTGGCCCATAGTGTAAATAAAGTTTACAGAAACCTT 5
|||||

RESULT 5
BM1719244
LOCUS BM1719244 733 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-E01-ajd-b-04-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
UI-E-E01-ajd-b-04-0-UI 5', mRNA sequence.
ACCESSION BM1719244
VERSION BM1719244.1 GI:19037818
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 733)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovey
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
     1..733
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="UI-E-E01-ajd-b-04-0-UI"
        /clone_lib="UI-E-E01"
        /tissue_type="fetal eye"
        /dev_stage="fetal"
        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
        /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
        modified polylinker; Site.1: EcoR I; Site.2: Not I;
        UI-E-E01 is a normalized cDNA library containing the
        following tissue(s): fetal eye. The library was

```


CONSTRUCTED according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the CCGTAT8 tail. The sequence tag for this library is CCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

BASE COUNT	199 a	115 c	150 g	267 t	2 others
ORIGIN					
Query Match	17.3%; Score 710.4; DB 14; Length 733;				
Best Local Similarity	99.4%; Pred. No. 2.3e-149;				
Matches 722; Conservative 0; Mismatches 3; Indels 1; Gaps 1;					
JY	3162	TGTAATAATTCCTTTAGCCCAATTTTTCTAGACTGTCTCTGTGGAAATATATTGTGTGTGTG	3221		
Dd	1	TGTAATAATTCCTTTAGCCCAATTTTTCTAGACTGTCTCTGTGGAAATATATTGTGTGTGTG	60		
QY	3222	ATATATGCATGTGTGTGATGTATGTATGGATTTAATCTAATCTAATAATTTGTGCCCGC	3281		
Dd	61	ATATATGCATGTGTGTGATGTATGTATGGATTTAATCTAATCTAATAATTTGTGCCCGC	120		
QY	3282	AGTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATGTTTCATCATGACAACCT	3341		
Dd	121	AGTGTGCCAAAGTGCATAGTCTGAG-TAAAAATCTAGGTGATGTTTCATCATGACAACCT	179		
QY	3342	GCTCAGTCCCAATTTAACCTGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTA	3401		
Dd	180	GCTCAGTCCCAATTTAACCTGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTA	239		
QY	3402	CCATTACAAATGGGATATAGAAGCAGCGTGAAGCAGATGAGCTGTGGACTAGCAATAT	3461		
Dd	240	CCATTACAAATGGGATATAGAAGCAGCGTGAAGCAGATGAGCTGTGGACTAGCAATAT	299		
QY	3462	AGGCTTTTGTGTGGTGGTGGTTGTGATAAGCAGTATTTGGGGTCAATATGTTTCCCTGT	3521		
Dd	300	AGGCTTTTGTGTGGTGGTGGTTGTGATAAGCAGTATTTGGGGTCAATATGTTTCCCTGT	359		
QY	3522	GCTGGAGCAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGT	3581		
Dd	360	GCTGGAGCAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCATGT	419		
JY	3582	GGTGATGAAATGGCCAGGTTGTCTGTATATTCTTTTCAGACTTCGCCACAGAGATTGCTGA	3641		
Dd	420	GGTGATGAAATGGCCAGGTTGTCTGTATATTCTTTTCAGACTTCGCCACAGAGATTGCTGA	479		
QY	3642	TAATAAATTAGGTAAGTATAATTTCTGGGCCATATTTTAGCACAGGTAATAATACATCAG	3701		
Dd	480	TAATAAATTAGGTAAGTATAATTTCTGGGCCATATTTTAGCACAGGTAATAATACATCAG	539		
QY	3702	GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGCTGTTAGCAGTCAA	3761		
Dd	540	GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGCTGTTAGCAGTCAA	599		
QY	3762	ATCTATTATTCCTACTGGCGCATCATATGCAAGTACTGATATGCCCTATATATAAGCCATAGG	3821		
Dd	600	ATCTATTATTCCTACTGGCGCATCATATGCAAGTACTGATATGCCCTATATATAAGCCATAGG	659		
QY	3822	TTACACCAATTTGTTTAGACAATTTGCTTTTTTTCAGATGCTGTTGTTCTTTTCATATG	3881		
Dd	660	TTACACCAATTTGTTTAGACAATTTGCTTTTTTTCAGATGCTGTTGTTCTTTTCATATG	719		
QY	3882	AAAAAA 3887 			
Dd	720	NRAAAA 725			

RESULT 6

BQ018994/c

LOCUS	BQ018994	777 bp	mRNA	linear	EST 27-MAR-2002			
DEFINITION	UI-H-DHI-awv-o-07-0-UI.sl NCI-CGAP_DHI Homo sapiens cDNA clone IMAGE:5824350 3', mRNA sequence.							
ACCESSION	BQ018994							
VERSION	BQ018994.1	GI:19754271						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	NCI-CGAP (bases 1 to 777) 1 - CGAP http://www.ncbi.nlm.nih.gov/ncicgap .							

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

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Location/Qualifiers
1. .777
/organism="Homo. sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5824350"
/clone_lib="NCI_CGAP_DHI"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DHI is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tag for this library is AGATCATTTGCC"

```

BASE COUNT	219 a	138 c	166 g	253 t	1 others
ORIGIN					
TAG_SEQ=AGATCATGTC"					
TAG_TISSUE=lung					
TAG_LIB=UI-H-DH1					

Query Match	17.2%;	Score 704.2;	DB 14;	Length 777;
Best Local Similarity	97.9%;	Pred. No. 5.9e-148;		
Matches 734;	Conservative	0;	Mismatches 14;	Indels 2;
				Gaps 2;

OY	1595	TTTGTGACCAAGAAATTTAAAAATTGTTTCAGTCATGCCTCGTGCTGCTGTTACCAG	1654
Ddb	750	TATNTGTGAGCAAGAATTTAAAATGTTTCCAGTCATGCCTCGTGCTGTTACCAG	691
OY	1655	TCAAAAGTCTCATCACCTCGGTCCCCTGAACGAAACAAGCATCCAGTGGAGAACCAC	1714
Ddb	690	TCCAAAAGTCTGATGACTCGGTCCCCATGACGGAACAAGCATCCAGTGGAGAACCAC	631
OY	1715	GATCAAAAACACCAACACACAGACCGGAGACGCCATAAGGACAGCATGAATGACCACCC	1774
Ddb	630	GATCAAAAACACCAACACACAGACCGGAGACGCCATAGGACAGCATGACTGACCACC	571
OY	1775	TTAAGACATCCTCGGTACTCCCAATAATCTCTCGGAGAAAAAATCACAAGGCAACTG	1834

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Db 570 TTAGAGCACTCTCTCGGTACTCCCAATAATCTCTCGGAGAAAAAATACAAAGCAACTG 511
QY 1835 TGACTCCGGGAATCTCTCTCTGATCCTTCTCTTAATCACTCCACACCAAGAAGA 1894
Db 510 TGAGTCGGGAATCTCTCTCTGATCCTTCTCTTAATCACTCCACACCAAGAAGA 451
QY 1895 AATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACTACAGATCGT 1953
Db 450 AATGCTTTCCAAAACCGGAAGGTAGACTGGTTTATCCACCCCAACATCTACGAATCGT 391
QY 1954 ACTTCTTTAATGATCAATTTACATPATCTCTGGTGTGTGTTATTCAGCAGCTAAAAAATGGT 2013
Db 390 ACTTCTTTAATGATCAATTTACATPATCTCTGGTGTGTGTTATTCAGCAGCTAAAAAATGGT 331
QY 2014 GGGAGCTGGGGAGATGAAGACTGTTAAATGAACACAGAGATATTTACTACTTTTGC 2073
Db 330 GGGAGCTGGGGAGATGAAGACTGTTAAATGAACACAGAGATATTTACTACTTTTGC 271
QY 2074 ATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGCGAGTTCTGGTGAATGTTCAA 2133
Db 270 ATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGCGAGTTCTGGTGAATGTTCAA 211
2134 TGGGAACCTGGTCACCATGAACCTTTAGAGATTAAACGACAAGATTTTCTACTTTTTTAAG 2193
Db 210 TGGGAACCTGGTCACCATGAACCTTTAGAGATTAAACGACAAGATTTTCTACTTTTTTAAG 151
QY 2194 TGA-TTTTTTGTCTTCAGCCAAACAAATATGGGTCAGGTCACATTTTATTTGAAATGT 2252
Db 150 TGATTTTTTTGTCTTCAGCCAAACAAATATGGGTCAGGTCACATTTTATTTGAAATGT 91
QY 2253 CATTTGGTGCCAGTATTTTAACTGCAATAGCCTAACATGATTTTGAACCTTATTT 2312
Db 90 CATTTGGTGCCAGTATTTTAACTGCAATAGCCTAACATGATTTTGAACCTTATTT 31
QY 2313 ACACATAGTTTGAACAAAAAAGACAAAAA 2342
Db 30 ACACATAGTTTGAACAAAAAAGACAAAAA 1

RESULT 7
LOCUS AUI39639
DEFINITION AUI39639 PLACE1 Homo sapiens cDNA clone PLACE1011029 5', mRNA
sequence.
ACCESSION AUI39639
VERSION AUI39639.1 GI:11001160
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 764)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1. 764
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1011029"

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/clone_lib="PLACE1"
/tissue_type="placenta"
/notes="Vector: pME18SFL3"
BASE COUNT 252 a 134 c 111 g 263 t 4 others
ORIGIN

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Query Match 17.0%; Score 695.8; DB 9; Length 764;
Best Local Similarity 97.6%; Pred. No. 4.6e-146;
Matches 726; Conservative 0; Mismatches 15; Indels 3; Gaps 2;
QY 2322 TTCAAAAAAGAGACAAAAATAGTATTCAGGTGAGCAATAGATTAGTATTTTCCACGT 2381
Db 5 TTTGAAAAAAGAGACAAAAATAGTATTCAGGTGAGCAATAGATTAGTATTTTCCACGT 64
QY 2382 CACTATTATTATTTTAAAAACACAAAAATCTTAAAGCTACAACTACTACAGGCCCTTAA 2441
Db 65 CACTGTTTATTTTAAAAACACAAAAATCTTAAAGCTACAACTACTACAGGCCCTTAA 124
QY 2442 AGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGTTTACTCAAAAGAAATTTTAA 2501
Db 125 AGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGTTTACTCAAAAGAAATTTTAA 184
QY 2502 ACTGTATTTTATTTTAAATGCTGTTTATTACAGGGGACCTTGAACATGTTTGTATG 2561
Db 185 ACTGTATTTTATTTTAAATGCTGTTTATTACAGGGGACCTTGAACATGTTTGTATG 244
QY 2562 TTAATTTCAAAAGCTAATGCTTCAATCAGATAGTTCCTTTTTCACAAAGTTCAATCTGTTT 2621
Db 245 TTAATTTCAAAAGCTAATGCTTCAATCAGATAGTTCCTTTTTCACAAAGTTCAAT-CTGTTT 303
QY 2622 TCAATGTAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTTAAATGTGTGTCAT 2681
Db 304 TCAATGTAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTTAAATGTGTGTCAT 363
QY 2682 TTAACCTCTGCTGAGACTTTTCACTGCACTGTATATAGAACTTAAACACACCTTAAGAGA 2741
Db 364 TTAACCTCTGCTGAGACTTTTCACTGCACTGTATATAGAACTTAAACACACCTTAAGAGA 423
QY 2742 AAAAGATCGAATTTTTCAGATGATTCGGAATTTTTCATTTCAGGTATTTGTAATAGTGACA 2801
Db 424 AAAAGATCGAATTTTTCAGATGATTCGGAATTTTTCATTTCAGGTATTTGTAATAGTGACA 483
QY 2802 TATATATGATATACATATACCTCTCTTCTTCTTAAATTTTGTAAAAATGTTTAACTGGC 2861
Db 484 TATATATGATATACATATACCTCTCTTCTTCTTAAATTTTCTTAAAAATGTTTAACTGGC 543
QY 2862 AGTAAGTCTTTTGTGATCATCTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG 2921
Db 544 AGTAAGTCTTTTGTGATCATCTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG 603
QY 2922 ATGAGTTTATCATGTGAGTGAATAAATTAATCCACAAATGCCACCAAGTAACCTTAACGAT 2981
Db 604 ATGAGTTTATCATGTGAGTGAATAAATTAATCCACAAATGCCACCAAGTAACCTTAACGAT 661
QY 2982 TCTTCACTTCTTGGGGTGTTCAGTATGAACCTAACTCCCAACCCCAACATCTCCCTCCCA 3041
Db 662 TCTTCACTTCTTGGGGTGTTCAGTATGAACCTAACTCCCAACCCCAACATCTCCCTCCCA 721
QY 3042 CATTTGCACCATTTTCAAGGGCCC 3065
Db 722 CATTTGCACCATTTTCAAGGGGNC 745

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RESULT 8
LOCUS A1694278/c
DEFINITION IMAGE:2331048 3', similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION A1694278
VERSION A1694278.1 GI:4971618
KEYWORDS EST.
SOURCE human.

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 739)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               This clone is available royalty-free through LNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Insert Length: 1706 Std Error: 0.00
               Seq primer: -400P from Gibco
               High quality sequence stop: 458.
FEATURES       Location/Qualifiers
               1..739
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Soares_NFL_T_GBC_S1"
               /lab_host="DH10B"
               /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
               a modified polylinker; Site_1: Not I; Site_2: Eco RI;
               Equal amounts of plasmid DNA from three normalized
               libraries (fetal lung NBHL19W, testis NHT, and B-cell
               NCI-CGAP_GCB1) were mixed, and ss circles were made in
               vitro. Following HAP purification, this DNA was used as
               tracer in a subtractive hybridization reaction. The driver
               was PCR-amplified cDNAs from pools of 5,000 clones made
               from the same 3 libraries. The pools consisted of
               I.M.A.G.E. clones 297480-302087, 682632-687239,
               726408-728711, and 729096-731399. Subtraction by Bento
               Soares and M. Fatima Bonaldo.
BASE COUNT     252 a 148 c 120 g 219 t
ORIGIN
Query Match    16.9%; Score 694.4; DB 9; Length 739;
Best Local Similarity 98.2%; Pred. No. 9.5e-146;
Matches 723; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 3370 CTTCTGCTCATTAATACTTGTGTAATCATGTTTACCATTACAAATGGGATATAAGAGGCAGC 3429
Db 739 CTTCCGCGATTTCAT-AATCCTGTATTATGTTT-CCTTCCAAATGGGATATAAGAGGCAGC 682
QY 3430 GTGAACGACAGTAGCTGCGACAGCAATATAGGTTTGTGTTGGTTGGTTGGTTGAT 3489
b 681 GTGAAGCAGACAGCTGTGCGACTACAAATATAGGTTTGTGTTGGTTGGTTGGTTGAT 622
QY 3490 AAAGCAGTATTGGGGTCATATTTCTCTGCTGGAGCAAAAGTCATTACACTTTTCAA 3549
Db 621 AAAGCAGTATTGGGGTCATATTTCTCTGCTGGAGCAAAAGTCATTACACTTTGAAA 562
QY 3550 GTATTATATGTTCTTATTCCTCAATCAATGTTGATGAATATGCCAGGTTGTCTGATA 3609
Db 561 GTATTATATGTTCTTATTCCTCAATTCATGTTGATGAATATGCCAGGTTGTCTGATA 502
QY 3610 TTCTTTTTCAGACTTCGCCAGACAGATTGCTGATATAATAATAGTAGATATAATTTGTTGG 3669
Db 501 TTCTTTTTCAGACTTCGCCAGACAGATTGCTGATATAATAATAGTAGATATAATTTGTTGG 442
QY 3670 GCCATATTTTAGGACAGTAAATAACATCAGTTTCCAGTTGCTGAATTCAGAGGTAA 3729
Db 441 GCCATATTTTAGGACAGTAAATAACATCAGTTTCCAGTTGCTGAATTCAGAGGTAA 382
QY 3730 GAAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACATGGCCGCATCATATG 3789
Db 381 GAAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACATGGCCGCATCATATG 322
QY 3790 CAGTGATATATGCGCTATATATATAGCCATAGGTTTCACACCATTTTGTGTAGACAATGTC 3849
Db 321 CAGTGATATATGCGCTATATATATAGCCATAGGTTTCACACCATTTTGTGTAGACAATGTC 262

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QY 3850 TTTTTCACAGATGCTTTGTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 3909
Db 261 TTTTTCACAGATGCTTTGTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 202
QY 3910 GTCATAGATTTCTGAAGCGTCGAAGTGCATTTTATTATGGAAGTGGTAGTAAGTGTGG 3969
Db 201 GTCATAGATTTCTGAAGCGTCGAAGTGCATTTTATTATGGAAGTGGTAGTAAGTGTGG 142
QY 3970 TTTTACTAGCAGGAATATTTCCTCAATTTCTACCTTTTACTACATCTTTTCAACAAGTAACCTT 4029
Db 141 TTTTACTAGCAGGAATATTTCCTCAATTTCTACCTTTTACTACATCTTTTCAACAAGTAACCTT 82
QY 4030 GTAGAAATGAGCCAGCAAGCCAGGCTGAGTTGGCAGTGGCCCATAGTGTAAATAATAA 4089
Db 81 GTAGAAATGAGCCAGCAAGCCAGGCTGAGTTGGCAGTGGCCCATAGTGTAAATAATAA 22
QY 4090 AGTTTACAGAAACCTT 4105
Db 21 AGTTTACAGAAACCTT 6

RESULT 9
BQ575745/c
LOCUS      BQ575745              732 bp      mRNA      linear      EST 19-JUN-2002
DEFINITION UI-H-E21-bbg-h-22-0-UI.s1 NCI-CGAP_Ch2 Homo sapiens cDNA clone
            UI-H-E21-bbg-h-22-0-UI 3', mRNA sequence.
ACCESSION   BQ575745
VERSION     BQ575745.1 GI:21479062
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 732)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitellis/ Rush Presbiterian, Dept. of
            Orthopaedics
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
POLYA-Yes.
FEATURES    Location/Qualifiers
            1..732
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="UI-H-E21-bbg-h-22-0-UI"
            /clone_lib="NCI-CGAP_Ch2"
            /tissue_type="Chondrosarcoma Grade II"
            /dev_stage="Adult"
            /lab_host="DH10B (Life Technologies)"
            /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
            with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
            NCI-CGAP_Ch2 is a normalized cDNA library containing the
            following tissue(s): Chondrosarcoma Grade II. The library
            was constructed according to Bonaldo, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pT73-pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (dT)18 tail. The sequence tag for this library is
            TGATCAGCCT.
            TAG_LIB=UI-H-E21

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|||||
Db 204 AAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTG 145
Qy 3967 TGGTTTACTAGCAGGAATATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACAAGTAAC 4026
Db 144 TGGTTTACTAGCAGACTATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACAAGTAAC 85
Qy 4027 TTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATTAAGTGTAAAT 4086
Db 84 TTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATTAAGTGTAAAT 25
Qy 4087 AAAAGTTTACAGAAACCTT 4105
Db 24 AAAAGTTTACAGAAACCTT 6

RESULT 11
-BO006584/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BO006584 705 bp mRNA linear EST 26-MAR-2002
IMAGE:5846029 3', mRNA sequence.
BO006584
BO006584.1 GI:19731484
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5846029"
/clone_lib="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dh)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG LIB-DT-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"
235 a 143 c 106 g 220 t 1 others
BASE COUNT
ORIGIN

Query Match
16.7%; Score 685; DB 14; Length 705;

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Best Local Similarity 99.9%; Pred. No. 1.2e-143;
Matches 685; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3420 AAGAGCGCGTGAAGCAGATCAGCTGCGACTAGCAATATATAGGTTTGTGGTTGG 3479
Db 705 AAGAGCGCGTGAAGCAGATCAGCTGCGACTAGCAATATATAGGTTTGTGGTTGG 646
Qy 3480 TTGGTTTGATAAAGCAGTATTTGGGGTGCATATTTTCCCTGCTGCGAGCAAAAGTCATT 3539
Db 645 TTGGTTTGATAAAGCAGTATTTGGGGTGCATATTTTCCCTGCTGCGAGCAAAAGTCATT 586
Qy 3540 ACACCTTGAAGTATATATTTGTTCTTATCCTCAATTCATGCTGATGAATTTGCCAGG 3599
Db 585 ACACCTTGAAGTATATATTTGTTCTTATCCTCAATTCATGCTGATGAATTTGCCAGG 526
Qy 3600 TTGCTGTATATTTCTTTCAGACTTCGCCAGACAGATGCTGATATAAATAGTAAAT 3659
Db 525 TTGCTGTATATTTCTTTCAGACTTCGCCAGACAGATGCTGATATAAATAGTAAAT 466
Qy 3660 AATTTGTTGGGCCATATTTTAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATT 3719
Db 465 AATTTGTTGGGCCATATTTTAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATT 406
Qy 3720 GCAAGCTAAGAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACCTGGC 3779
Db 405 GCAAGCTAAGAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACCTGGC 346
Qy 3780 GCATCATATGCACTGATATATGCTTATTAATGAAGCATAGGTTACACCATTTTGTGTTA 3839
Db 345 GCATCATATGCACTGATATATGCTTATTAATGAAGCATAGGTTACACCATTTTGTGTTA 286
Qy 3840 GACAATGCTCTTTTTCAGATGCTTTTCTTTCATATGAAAAAATGCAATTTATA 3899
Db 285 GACAATGCTCTTTTTCAGATGCTTTTCTTTCATATGAAAAAATGCAATTTATA 226
Qy 3900 AATTCAGAAAGTCATAGATTTCTGAAGCGTCAACGTCATTTTATTTATGGACTGTA 3959
Db 225 AATTCAGAAAGTCATAGATTTCTGAAGCGTCAACGTCATTTTATTTATGGACTGTA 166
Qy 3960 GTAACTGTGGTTTACTAGCAGGAATATTTCCAAATTTTCTACCTTTACTACATCTTTCAAC 4019
Db 165 GTAACTGTGGTTTACTAGCAGGAATATTTCCAAATTTTCTACCTTTACTACATCTTTCAAC 106
Qy 4020 AGTAACTTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATAAAT 4079
Db 105 AGTAACTTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATAAAT 46
Qy 4080 GTAAATATAAAGTTTACAGAAACCTT 4105
Db 45 GTAAATATAAAGTTTACAGAAACCTT 20

RESULT 12
BG116534
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BG116534 742 bp mRNA linear EST 30-JAN-2001
602317633F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:441905 5',
mRNA sequence.
BG116534
BG116534.1 GI:12610040
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10151 row: e column: 10
 High quality sequence stop: 697.

FEATURES

source
 1. 742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4417905"
 /clone_lib="NIH_MGC_88"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: small intestine; Vector: pCMV-SPORT6;
 Site: 1; Notif: Site 2; Sali: Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."
 BASE COUNT 166 a 211 c 208 g 157 t
 ORIGIN
 Query Match 16.6%; Score 683; DB 12; Length 742;
 Best Local Similarity 97.1%; Pred. No. 3.5e-143;
 Matches 706; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
 QY 31 GTGGAGTGAAGGCTGGAGCTTTGGAGGAGACGGGAGGAGACTGGAGCGGTTC 90
 Db 1 GTGGAGTGAAGGCTGGAGCTTTGGAGGAGACGGGAGGAGACTGGAGCGGTTC 60
 QY 91 CTCGGAGTTTCTTTTCGTCGGAGCCCTCGCGCGGCTACAGTCATCCCGCTGCT 150
 Db 61 CTCGGAGTTTCTTTTCGTCGGAGCCCTCGCGCGGCTACAGTCATCCCGCTGCT 120
 QY 151 GACGATTGTGAGAGCGGTGGAGAGGCTTCATCCATCCACCGCTCTGCGCGGGAT 210
 Db 121 GACGATTGTGAGAGCGGTGGAGAGGCTTCATCCATCCACCGCTCTGCGCGGGAT 180
 QY 211 TGGGTCCAGCGACACCTCCCGGGAGAGAGAGTGCAGGAGTTTCTGAAGCGGG 270
 Db 181 TGGGTCCAGCGACACCTCCCGGGAGAGAGAGTGCAGGAGTTTCTGAAGCGGG 240
 QY 271 GAAGTGTGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
 Db 241 GAAGTGTGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 331 CCACCCACCTCGCTTTCTCCGCTTCTCTGCGCCAGCGCGCGCGCGCGCGCGCG 390
 Db 301 CCACCCACCTCGCGCTTCTCTGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 391 GTCTCGGACGCGCGAGCTCCACGGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 450
 Db 361 GTCTCGGACGCGAGCTCCACGGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 420
 QY 451 GCAATAGAGATATTTCTCAATTTGCTCAAGATGGAACCCCTTGCTCAGGGCATC 510
 Db 421 GCAATAGAGATATTTCTCAATTTGCTCAAGATGGAACCCCTTGCTCAGGGCATC 480
 QY 511 CTTTGGCTGGCAGTGGTGGATGATATCATGATATCTGAGAGATACAGACACAA 570
 Db 481 CTTTGGCTGGCAGTGGTGGATGATATCATGATATCTGAGAGATACAGACACAA 540
 QY 571 TCTAAGCAATCATGTTGGATGATTTTCCACCATTTTCTGTCGACAGAGCTCAGTTCCTG 630
 Db 541 TCTAAGCAATCATGTTGGATGATTTTCCACCATTTTCTGTCGACAGAGCTCAGTTCCTG 600
 QY 631 TACCACATCAACCCACTAATTTGGTCTTACCCAGCAATGGCTCAATGCACAACTATTG 690
 Db 601 TACCACATCAACAA-CCACTAATTTGGTCTTACCCAGCAATGGCTCAATGCACAACTATTG 659
 QY 691 CCCACAGAGACTAAATTTACTTCAGCTTTCAATACATTTACACTGTGATATCTTGATC 750
 Db 660 CCCACAGAGACTAAATTTACTTCAGCTTTCAATACATTTACACTGTGATATCTTGATC 719

QY 751 TATTTC 757
 Db 720 CTATTTC 726

RESULT 13

LOCUS BG699589 771 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602679314F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4812050 5',
 mRNA sequence.
 ACCESSION BG699589
 VERSION BG699589.1 GI:13968056
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 771)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10703 row: 1 column: 03
 High quality sequence stop: 748.

FEATURES

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 1. 771
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 /clone="IMAGE:4812050"
 /clone_lib="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: Sali-XhoI (gtcgaag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
 size-selected for average insert size 2.5 kb and
 normalized to 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 182 a 224 c 198 g 167 t
 ORIGIN

Query Match 16.6%; Score 683; DB 12; Length 771;
 Best Local Similarity 97.4%; Pred. No. 3.5e-143;
 Matches 747; Conservative 0; Mismatches 15; Indels 5; Gaps 5;

QY 134 AGTCATCCCGCTGGTCTGACGATTGTGGAGAGCGGTGGAGAGCTTCATCCATCCACC 193
 Db 6 AGTCATCCCGCTGGTCTGACGATTGTGGAGAGCGGTGGAGAGCTTCATCCATCCACC 65
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 VERSION AI953824.1 GI:5746134
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 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 (CGAP/BTGA), Tumor Gene Index
 Unpublished (1998)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: c9apbs-remail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
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 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
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 Library constructed by Life Technologies."
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 Best Local Similarity 96.4%; Pred. No. 1.7e-136;
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Search completed: December 12, 2002, 14:25:46
 Job time : 5005 secs

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RESULT 2

US-09-919-497-12
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 ; Patent No. US20020106662A1
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 ; APPLICANT: Mutter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/7225
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/221,735
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 2595
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-919-497-12

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Db 2174 CATATGCAGTATATATGCTTATAATATAAGCCATAGGTTACACCATTTTGTATTAGACA 2233
QY 3844 ATGTCCTTTTTCAGATGCTTTGTTCTTCTCATATGAAAAATGCAATTTTATAAAT 3903
Db 2234 ATGTCCTTTTTCAGATGCTTTGTTCTTCTCATATGAAAAATGCAATTTTATAAAT 2293
QY 3904 CAGAAAGTCATAGATTCTGAAGGCTCAACGTGCAATTTTATTATGAGTGGTAA 3963
Db 2294 CAGAAAGTCATAGATTCTGAAGGCTCAACGTGCAATTTTATTATGAGTGGTAA 2353
QY 3964 CTGTGTTTACTAGCAGGAATATTTCCAAATTTCTTACTTACTACATCTTTTCAACAAGT 4023
Db 2354 CTGTGTTTACTAGCAGGAATATTTCCAAATTTCTTACTTACTACATCTTTTCAACAAGT 2413
Y 4024 AACTTTGTAGAAATGAGCCAGAGCCAGGCCCTGAGTTGGCAGTGGCCCAATAAGTGTA 4083
Db 2414 AACTTTGTAGAAATGAGCCAGAGCCAGGCCCTGAGTTGGCAGTGGCCCAATAAGTGTA 2473
QY 4084 AATAAAAGTTTACAGAAACCTT 4105
Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 3
US-09-931-157-2
; Sequence 2, Application US/09931157
; Patent No. US200200824141
; GENERAL INFORMATION:
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

Query Match 9.6%; Score 395.8; DB 10; Length 4301;
Best Local Similarity 65.7%; Pred. No. 6.8e-84;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

QY 689 TGCCACAGCAGACATAAATTTACTTCAGCTTTCAAAATACATTAACACTGTGATATCTGT 748
Db 505 TGCCAAAGACCCATCGAGATCAAGAGACTTTCAAAATACATCAACCGGTTGTGCTCGC 564
QY 749 ACTATTTTCATCGTGGGAATGTTGGGGAATGCACTCTGCTCAGGATCATTTTACCAGAAC 808
Db 565 CTGTGTTTCGTGGGATCATCGGAACCTCCACACTCTCAGAAATATCTACAGAAC 624
QY 809 AAATGTATGAGAAATGCGCCCAACGCGTGTAGCCAGTCTTGCCCTTGGAGACCTTATC 868
Db 625 AAGTGCATGCGAAACGGTCCCAATATCTGTATGCGCAGCTTGGCTCTGGAGACCTGCTG 684
QY 869 TATGTGGTCATGATCTCCCTCATCAATGATTTAAGTGTGCTGGCTGGCGGCTGGCCCTTT 928
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Db 685 CACATGCTCATTTGACATCCCTATCAATGTCTACAAGCTGTGCAGAGAGCTGCC----- 740
QY 929 GATCACAAATGACATTTGGCGTATTTCTTGAAGCTGTTCCTCTTTTTCGAGAGCTCCTCG 988
Db 741 -----ATTGGAGCTGAGATGTGTAAGCTGGTCTTTTCATACAGAAAGCTCC 789
QY 989 GTGGGATCACCCCTCCCTCAACCTCTGCGCTCTTAGTCTTGACAGGTACAGAGCAGTTGCC 1048
Db 790 GTGGGATCACTGCTGCTGAGTCTATGTGCTCTGAGTATTCACAGATATCAGAGCTGTGCT 849
QY 1049 TCTGTGAGTCTGCTTTCAGGGAATTTGGAATTCCTTTGTAATTCGCAATTTGTAATTCCTCC 1108
Db 850 TCTGTGAGTATTAAGGAATTTGGGTTCCAAATTTGACAGAGCAGTAAATTTGTTTG 909
QY 1109 ATCTGATCTGCTCTTATCTCTGGCCATTCCTTGAAGCGATTTGGCTTCGTCATGGTACCC 1168
Db 910 ATTTGGTGGTCTCTGCTGCTTCTGCTTCCCTGAAGCCATAGGTTTGTATATAATTAAC 969
QY 1169 TTTGAATATAGGGGTCAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 970 ATGGACTACAAGGAAGTTATCTGCGAATCTGCTTCTCATCCCTTCAGAGAGACGCT 1029
QY 1223 TTCATGGAGTTTACCAAGATGTAAAGGACTGGTGGCTCTTTCGGGTCTTATTTCTGTATG 1282
Db 1030 TTCATGCACTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTCTATTTCTGCTTG 1089
QY 1283 CCCTTGGTGTGCACTCGCATCTTCTACCCCTCATGCTTGTGAGATTTGTAACAGAGAG 1342
Db 1090 CCATTTGGCCATCACTGCTCAATTTTATACACTAATGACCTGTGAAATTTG---AGAAAG 1146
QY 1343 AATGGCAGCTTGAGAAATTCCTTCAGTGAACATCTTAAGCAGCGTCGAGAGTGGCAAAA 1402
Db 1147 AAAAGTGGCATGCAGATTTCTTAAATGATCACCTAAGCAGAGACGGGAAGTGGCCAAA 1206
QY 1403 ACAGTTTCTGCTGCTGCTGCTTAAATTTTGTCTTTTGTGCTTCTTCTTCTTCACTTAAGCCGT 1462
Db 1207 ACCGCTTTTGGCTGGCTGCTGCTTGTCTTTGGCTCTGCTTGGCTTCCCTTCACTCAGCAGG 1266
QY 1463 ATATTGAAGAAACTGTGTATAACGAAATGGCAAGAACCGATGTGAATTTACTTAGTTTC 1522
Db 1267 ATTTGAAGCTCACCTCTTTTATAATCAAGATGATCCCAATAGATGTGAACCTTTTGAAGCTTT 1326
QY 1523 TTACTGCTCATGATACATCGGTATTAATTAATTTGGCAACCAATGAATTCATGATATAAACCC 1582
Db 1327 CTGTTGGTATTTGGACTATATTTGATCAACATGGCTTCACTGAATTTCTGCTTAAACCCA 1386
QY 1583 ATAGCTCTGATTTTGTGAGCAAGAAATTTAAAAATTTGTTTCCAGTCATCCCTCTGCTGC 1642
Db 1387 ATGCTCTGATTTTGGTGAAGCAAAAGATTCAAAAAAGTCTTTTAACTGCTTATGCTGC 1446
QY 1643 TGCTG 1647
Db 1447 TGGTG 1451
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```
RESULT 4
US-09-867-701-3320
; Sequence 3320, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3320
; LENGTH: 438
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i TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(438)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-3320

Query Match 6.9%; Score 284.4; DB 10; Length 438;
Best Local Similarity 89.1%; Pred. No. 4.9e-58;
Matches 383; Conservative 0; Mismatches 34; Indels 13; Gaps 7;

QY 1577 AACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTGTTCCAGTCATGCCCTC 1636
Db 9 AACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTGTTCCAGTCATGCCCTC 68

QY 1637 TGCCTGCTCTGTACACAGTCCAAAGTCTGTAGCTCGGTCCCATGAACGGAACAAGC 1696
Db 69 TNCCTGCTCTGTACACAGTCCAAAGTCTGTAGCTCGGTCCCATGAACGGAACAAGC 128

QY 1697 ATCCAGTGAAGAACCCAGCATCAAAACCAACACACAGACCGGAGGAGCCATAAGGAC 1756
Db 129 ATCCAGTGAAGAACCCAGCATCAAAACCAACACACAGACCGGAGGAGCCATAAGGAC 188

QY 1757 AGCATGAACACACACCCCTTAGAGCACTCTCGGTACTCCCATATCTCTCGGA-GAA 1815
Db 189 AGCATGAACACACACCCCTTAGAGCACTCTCGGTACTCCCATATCTCTCGGA-GAA 248

QY 1816 AAAATACACAGGCAACGTGA--CTCCGGGAATCTTCTCTGAT--CCTTCCTCCTTA 1871
Db 249 AAAATACACAGGCAACGTGAAGTCCGGGAATCTTCTCTGAT--CCTTCCTCCTTA 308

QY 1872 ATTCACCTCCCAACCAAGAA--GAAATGCTTTCCAAACCGCAAGTAG--ACTGGTT 1926
Db 309 ATTCACCTCCCAACCGAGGAATGTTTCCAAACCGNAAGGTGGAGCTGGTT 368

QY 1927 TATCACCAACAACA-TCTAGCAATCGTACTCTTT--AATGATCTAATTTACATATTC 1983
Db 369 TTTCCACCAACAACATTTAGGATTCGTACTCTTTAATTTGGTTCTTAATTTACATATTC 428

QY 1984 TGCCTGTGT 1993
Db 429 TGCCTGTGT 438

RESULT 5
US-09-954-531-917/c
; Sequence 917, Application US/09954531
; Patent No. US20020165180A1
--GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cando
; FILE REFERENCE: Gene Sets
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 917
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Query Match 3.6%; Score 147; DB 9; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 1301 ATCTTCTACACCCCTCATGACTTGTGAGATGTTGAACAGGAAGTGGACGCTTGAGAAAT 1360
Db 468 ATTTTATACACTAANGACCTGTGAATGTTGAGAAGAAAGTGGCATGCGAGATTGCT 409

QY 1361 GCCCTCAGTGAACATCTTAAGCAGCGTTCGAGAGTGC---AAAAACAGTTTTCTGCTTG 1417
Db 408 TTAATGAGCACCCCTAAAGCCAGAGCCGNAAGTGGCCCAAAANCCGGTCTTTTGCCTG 349

QY 1418 GTTGAATTTTGTCTTTTGGTTCCTCTTCACTTAAGCCGTATATTAAGAAAAACT 1477
Db 348 GTTCTGGTCTTTTGGTTCCTCTTCACTTAAGCCGTATATTAAGAAAAACT 289

QY 1478 GTGTATACGAATGGACAAAGCAACGATGTGAATTTACTTTAGTTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATAATCAGATGATCCCAATAGATGTGAATTTTGAAGCTTTCTGTTGGTATTGGAC 229

QY 1538 TACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATT 1597
Db 228 TATATTGGTATCAACATGGCTTCACTGAATTCCTGCAATTAACCCAAATGCTCTGTATT 169

QY 1598 GTGAGCAAGAAATTTAAATTTGTTTCCAGTCATGCTCTGCTGTGCTG 1647
Db 168 GTGAGCAAGAAATTTAAATTTGTTTCCAGTCATGCTCTGCTGTGCTG 119

RESULT 6
US-09-962-436-531/c
; Sequence 531, Application US/09962436
; Patent No. US20020081301A1
--GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 531
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-962-436-531

Query Match 3.6%; Score 147; DB 10; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 1301 ATCTTCTACACCCCTCATGACTTGTGAGATGTTGAACAGGAAGTGGACGCTTGAGAAAT 1360
Db 468 ATTTTATACACTAANGACCTGTGAATGTTGAGAAGAAAGTGGCATGCGAGATTGCT 409

QY 1361 GCCCTCAGTGAACATCTTAAGCAGCGTTCGAGAGTGC---AAAAACAGTTTTCTGCTTG 1417
Db 408 TTAATGAGCACCCCTAAAGCCAGAGCCGNAAGTGGCCCAAAANCCGGTCTTTTGCCTG 349

QY 1418 GTTGAATTTTGTCTTTTGGTTCCTCTTCACTTAAGCCGTATATTAAGAAAAACT 1477
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Db 348 GTCTGGTCTTTGGCCCTGTGGCTTCCCTTCCCTCAGCAGGATTCGAAGCTCACT 289
QY 1478 GTGTATACGAAGTAAAGCAAGCAGATGTGAATTTACTTAGTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATATCAGATGATCCCAATAGATGTAACCTTTTGAGCTTTCTGTGGTATGGAC 229
QY 1538 TACATCGGTATTAATCTGGCAACCATGAATTCATGTATATAACCCCATGCTGTATTTT 1597
Db 228 TATATGTTTCAACATGGCTTCACTGAATTCCTGCAATTAACCCCAATGCTGTATTTG 169
QY 1598 GTGACGAGAAATTAATAATTTTCCAGTCATGCTCTGCTGTGCTG 1647
Db 168 GTGACGAGAAATTAATAATTTTCCAGTCATGCTCTGCTGTGCTG 119

RESULT 7
-US-09-880-107-2060/c
Sequence 2060, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2060
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(592)
OTHER INFORMATION: n = a or c or g or t

US-09-880-107-2060
Query Match 3.6%; Score 147; DB 10; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;
QY 1301 ATCTTCTACACCCCTCATGACTTTGTGAGATGTTGAACAGAGAAATGGCAGCTTGAGAAAT 1360
Db 468 ATTTTATACACTTAAGACACCTGTGAATGTTGAGAGGAAAGTGGCATGCAGATTGCT 409
QY 1361 GCCCTCAGTGAATCTTAAGCAGCGTGCAGAGTGGC---AAACACAGATTTTCTGCTTG 1417
Db 408 TTAATAGACACCCCTTAAGCAGCGGAGGNAAGTGGCCCAAAACCCGCTTTTGGCCTG 349
QY 1418 GTTGTAATTTTGTCTTTGCTGTTGCTCTTCCCTTCACTTAAGCCGTATATTAAGAAACT 1477
Db 348 GTCTGTGCTTTGGCCCTGTGGCTTCCCTTCCCTCAGCAGGATTCGAAGCTCACT 289
QY 1478 GTGTATACGAAGTAAAGCAAGCAGATGTGAATTTACTTAGTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATATCAGATGATCCCAATAGATGTAACCTTTTGAGCTTTCTGTGGTATGGAC 229
QY 1538 TACATCGGTATTAATCTGGCAACCATGAATTCATGTATATAACCCCATGCTGTATTTT 1597
Db 228 TATATGTTTCAACATGGCTTCACTGAATTCCTGCAATTAACCCCAATGCTGTATTTG 169
QY 1598 GTGACGAGAAATTAATAATTTTCCAGTCATGCTCTGCTGTGCTG 1647
Db 168 GTGACGAGAAATTAATAATTTTCCAGTCATGCTCTGCTGTGCTG 119

RESULT 8

US-09-778-927A-27
Sequence 27, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 800
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(800)
OTHER INFORMATION: n = a,c,g,t any unknown or other

US-09-778-927A-27

Query Match 2.8%; Score 114.6; DB 10; Length 800;
Best Local Similarity 67.2%; Pred. No. 1.4e-17;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 689 TGCCACAGCAGACTAAATTTACTTTCAGCTTTCAATATACATTAACACTGTGATATCTTGT 748
Db 505 TGCCAGGACCCATCGAGATCAAGGAGACTTTCAATATACATCAACAGGTTGTGCTCTGC 564
QY 749 ACTATTTTCATCGTGGGAATGTTGGGAATGCAACTCTGCTCAGGATCAATTTACAGAAC 808
Db 565 CTGTGTTCTGCTGGGATCATCGGGAACCTCCACACTTCTGAGAATTTATCTACAAGAAC 624
QY 809 AAATCTATGAGGAATGGCCCAACGCGCTGATAGCCAGTCTTCCCTTGGAGACCTTATC 868
Db 625 AAGTCATGCGAAGACGGTCCCAATATCTTGTATCGCCAGCTTGGCTCTGGAGACCTGCTG 684
QY 869 TATGTGTCATGATCTCCCTATCAATGATTTAAGCTGCTGGGCGCTGGCCTTTT 928
Db 685 CACATCGTCATTTGACATCCCTATCAATGCTACAAAGCTGCTGCAGAGGACTGGCCATTT 744
QY 929 G 929
Db 745 G 745

RESULT 9
US-09-160-116-11
Sequence 11, Application US/09160116A
Patent No. US20010014457A1
GENERAL INFORMATION:
APPLICANT: Spindel, Elliot R.
APPLICANT: Nagalla, Srinivasa
APPLICANT: Barry, Brenda
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
FILE REFERENCE: 00537/098003
CURRENT APPLICATION NUMBER: US/09/160,116A
CURRENT FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 08/910,098
PRIOR FILING DATE: 1997-08-12
PRIOR APPLICATION NUMBER: US 08/279,590
PRIOR FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11


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; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1198)
US-09-160-116-11

Query Match      1.7%; Score 68.4; DB 10; Length 2595;
Best Local Similarity 46.1%; Pred. No. 2.6e-06;
Matches 412; Conservative 0; Mismatches 446; Indels 36; Gaps 4;

QY 761 GTGGGAATGTTGGGAATCAACTGCTCAGGATCATTTACACAGACAATGTATCAGG 820
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GTGGGATCCTCGGAATGCTATCCCTCAATCAAGACTCTTTTCAAGACTAAATCCATGCAA 238
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 821 AATGGCCCAACCGGTGATAGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCATT 880
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 ACAGTTCCAAATATTTTCATCACCAGCTGGCTTTTGGAGATCTGTTACTCTGCTGACT 298
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 881 GATCTCCCTATCAATGATTTAAGCTGTGGCTGGCGGTGGCCCTTTTGTATCACAAATGAC 940
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 TGTGTGCCAGTGGATGCAACCCACTACCTGGCAGAGGATGGCTTTTGGAAAGGTCGG- 357
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 941 TTTGGGGTATTTCTTTCGAGCTGTTCCCTTTTTCAGAGTCTTCGGTGGGGATCAC 1000
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 -----TTGTAAGTGGCTTTCTTCATCCGGCTCACTTCTGTCGGTGTATCA 403
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1001 GTCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCACTTGCCTCTGGATCGT 1060
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GTGTCACGCTAACAAATCTCAGCGTACAGATCAAGAGCACTGCTGAGCCACTTGAA 463
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1061 GTTCAGGGAATTTGGGATTCCTTTTGTGTAAGTCCATTTGAAATTTGCTTCCATCTGGATCCCTG 1120
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CGACAGCCCTCCAAATGCCATCTTGAAGACCTGTGCCAAAGCTGGTGCATCTGATCATG 523
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1121 TCCTTTATCTCGGCATTTCTCAGCGATTTGGCTGCTCATGATACCTTTTGAATATAGG 1180
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 GCTATGATTTTGTCTGTGCAAGGCTATTTCTCAAAATGTATACACTTTTCCAAGATCCT 583
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1181 GGTGAACAGCATAAACCTGTATGTCTCAATGCCACATCAAAATTCATGAGTTCTACCAA 1240
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 AACAGAAAGCTAACATTTGAATCCTGTACTCTTACCCTATCTCTGAGAGGCTTTTGACAG 643
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1241 GATGTAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGGG 1300
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 GAAATACATTTCTCTGTGTGTTTCTTGTGTGTTCTACATTATCCCGCTCTCGATTATCTCT 703
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1301 ATCTTCTACACCTCATGACTTGTGAGATGTTGAACAGAGGAATGGGAGCTTGAGAATT 1360
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 GTCATATTATTTGATTCGCCAGGACTCTTTTACAAAGCAACCTTGAACATACCGACTGAG 763
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1361 GCCCTCAGTGAACATCTTTAAGCAGCGCTCGAGA-----AGTGCAAAAACAGTTTTC 1411
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 GAACAAAGCCATGCCCGGAAGCAGATTGAATCCCGGAAGAGAAATGCCAAACGGTACTG 823
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1412 TCGTTGGTTGAATTTTGTGCTCTTTGCTGGTTCCTTCTTCACTTAAGCCGATATATGAG 1471
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 GTGCTGGTGGCTCTGTGCGACTCTGTGCTGGTTCGGAATCACT--CCTGTATCTCTATC 881
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1472 AAAACTGTATACGAATATGACAAAGAACCGATGTGAATTACTTAAGTTTCTTACTGCTC 1531
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 882 ACTCATTCACATTTATGAAGACTACGAGAGCCCTTCTGATGTCCCTTTGTCGTCACCAATT- 940
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1532 ATGGAATTACATCGGTATTAACTTTGCAACCACTGAATTCATGATATAACCCCACTGCTG 1591
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 941 -----TTCTCTCGGGTGTGCTTTTCAAGTAATCTCGGTGAACCCCTTTGCTGTG 991
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1592 TATTTTGTGACCAAGAAATTTAAATATTTTCCAGTCACTGCTCTGCTGCTG 1645
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 992 TATTGGCTGAGCAAGACCTTCCAGAGCATTTTAAAGGCTCAGCTCTGCTGCTC 1045
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10
US-09-160-116-1
; Sequence 1, Application US/09160116A
; Patent No. US20010014457A1
; GENERAL INFORMATION:
; APPLICANT: Spindel, Elliot R.
; APPLICANT: Negalla, Srinivasa
; APPLICANT: Barry, Brenda
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
; FILE REFERENCE: 00537/098003
; CURRENT APPLICATION NUMBER: US/09/160,116A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 08/910,098
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: US 08/279,590
; PRIOR FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Bombina bombina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)...(1319)
US-09-160-116-1

```

```

Query Match      1.5%; Score 62; DB 10; Length 1563;
Best Local Similarity 45.3%; Pred. No. 6.4e-05;
Matches 331; Conservative 0; Mismatches 375; Indels 24; Gaps 2;

QY 735 CTGTGATATCTTCTACTATTTTTCATCTGTGGGAATGTGGGAATGCAACTCTGCTCAGGA 794
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 CTGTACATATGCTGTATTTTCTGTGCGTATCTTGGAAACACAACTACTTATAAAG 399
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 795 TCATTTACCAGAAACAAATGTATGAGGAATGGCCCAACGCGCTGATAGCCAGCTTTGCC 854
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 TATTTTAAAAATCAAGTCAATGCAGACTGTTCTTAATATTTTCATCACCAGCTGCTT 459
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 855 TTGGAGACCTTATCTATGTGGTCATTTGATCTCCCTCATATGATTTTAAGCTGCTGCTG 914
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 TTGGAGATCTTCTTCTACTGCTGACCTGGCTGCCAGTGGACGATCTCGGTATATTGTGG 519
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 915 GCGCTGTGGCTTTTGTATCAATGACTTTTGGCGTATTTTTCGAAAGCTTCCCTCTTTT 974
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 ACAGCTGGATTTTGGAGAGCTGGCTGT-----AGATAATTTCTCTCA 564
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 975 TCGAGAAGTCTCGGGTGGGATCACCGTCTCTCAACCTCTGCGCTCTTAGTGTGACAGGT 1034
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 TACAGCTTACCTCTGTGCGAGTGTGCTGTACTTTAACTGTCTCAGTACTGACAGGT 624
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1035 ACAGAGCACTTGCCTCTGAGTGTGTTTCAGGAATTTGGGATTCCTTGTGTAACGCCA 1094
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 625 ACAGAGCACTTGTGAACCCCTTGAACCTTCAGACCTTCAGATGCCGTTTGAAGACATGTG 684
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1095 TTGAATTTCTCCATCTGATCTCTCTTTTCTCTGCGCAATTCCTGAGCGATTTGGCT 1154
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 GCAAGCTGTTTGTGTTTGGATCAATTTCCATGCTCTCTGCTGCTCCAGAGCTGTGTTCT 744
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1155 TCGTATGTCACCTTTTGAATATAGGGGTGAACAGCATAAAAACCTGTATGCTCAATGCCA 1214
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CAGATTTGTATGAATTTGGCAGCTCGAAAAAATAACCACTTTTGAAGCTGTGCTCCAT 804
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1215 CATCAAAATTCATGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTTATT 1274
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 805 ATCCAGTCTCTGAAAGATTTCTGCAAGAGACACATTTCCCTAATATGCTTCTCTGGTATCT 864
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1275 TCTGTATGCCCTTGTGTGCTGCTGCTCTTCTACACCTCATGACTTGTGAGATTTGA 1334
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 865 ACATTTGTTCCCTGTCAATCATTTCTGATATTAATCTTCTTATGCAAAACCCCTGTACA 924
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1335 A-----CAGAAAGGAATGGCAGCTTGGAGAAATTCCTCAGTGAACATCTTAAGCAGC 1385
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db 975 AAAGTACTTTCAACATGCTGCTGAGAGCACACTCACGCCGGAACAGATAGATCGC 984
Qy 1386 GTCGAGAGTGGCAAAACAGTTTTCTGCTGGTGTAAATTTTCTGCTGCTGGTTC 1445
Db 985 GCAACAGAGTGGCAAAACAGTGTGCTGGTGGCGCTATTGCTGCTGTTGGCTCC 1044
Qy 1446 CTCTTCACCTT 1455
Db 1045 CTAACACAT 1054

RESULT 11
US-09-960-352-4584
; Sequence 4584, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 2001-09-24
; SEQ ID NO 4584
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584

Query Match 1.3%; Score 54; DB 10; Length 416;
Best Local Similarity 45.8%; Pred. No. 0.0023;
Matches 186; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 2243 TTGGAATGCTATTTGGTGGCGAGTATTTTAACTGCATATAGCCAAACATGATTATTT 2302
Db 1 TTTTGTGTTTGG 60

Qy 2303 GAACCTATTACACATAGTTTGAAGAAAAAGACAAATAGTATTCAGGTGACCAAT 2362
Db 61 TATTAAATGAAAAATAGAAAAATAATA 120

Qy 2363 AGATTAGTATTTCCAGCTGCTATTTATTTTAAACACAAATCTTAAGCTACAAAC 2422
b 121 AAAAAATFAATTTTTTATAAAAAAAATAAAATTAATAAAAAAAATAAAAAAAATAAAAA 180

Qy 2423 AAATACCTACAGGCGCTTAAAGCACAGTCTGATGACATTTGGCAGTTTAAATAGATGTTA 2482
Db 181 AAAAAAGATTTTAAAAATTAATAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATA 240

Qy 2483 CTCAGAAGATTTTAAAGAACTGATTTTATTTTAAATGGTGTATTATTAACAGGAC 2542
Db 241 AAAAAAAATTTTAAATTTTAAAGAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 300

Qy 2543 CTGGAACATGTTTGTATGATTAATTCAAAGTAATCTCAATCAGATAGTTCTTTTTC 2602
Db 301 ATAGAAGATATAAAAAAGATTTTATTAATAATAATAATTTTAAATAATAATATGATGGTAATTT 360

Qy 2603 ACAAGTTCATCTGTTTTCATGTAATTTTGTATGATAAAATCAA 2648
Db 361 TATAAATTAATAAATTTTATAATAAATAATTTTAAATTAATAAAAAA 406

RESULT 12
US-09-804-551B-33
; Sequence 33, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects

; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618.4
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1518)
; NAME/KEY: n
; LOCATION: 1521
; OTHER INFORMATION: n is a or g or c or t/u, unknown, or other
US-09-804-551B-33

Query Match 1.2%; Score 50.2; DB 10; Length 1521;
Best Local Similarity 48.5%; Pred. No. 0.04;
Matches 216; Conservative 0; Mismatches 208; Indels 21; Gaps 2;

Qy 725 TACATTAACTGTGATATCTTTGTACTATTTTCATGCTGGGAATGGTGGGAATGCAACT 784
Db 208 TACATTGTACGGTGTGTACACGCTCATCTTCATTTGTGGAGTTTGGGCAACGGCAGC 267

Qy 785 CTGCTCAGGATCATTTTACCAGAAATATGATGAGGAATGGCCCCAACGCGTGATAGCC 844
Db 268 TGTGTCATCATCTCTTTTCGCCACCGCTCCATGCGCAACATACCCAAACACATACATCTT 327

Qy 845 AGCTTTGCCCTTGGAGACCTTATCTATGTGGTCATGATCTCCCTATCATGATTTTAAG 904
Db 328 TCACGTGGCCCTGGGTGATCTGTGTTTATTTATTTGTTGTGTACCTGTGCCACGATTTGC 387

Qy 905 CTGCTGGTGGCGCTGGCTTTTGTATCACAATGACTTTTGGCGTATTTCTTTGCAAGCTG 964
Db 388 TACACGCAAGAAAGCTGGCCCTTTCAGCGGAACA-----TGTCGCCATC 432

Qy 965 TTCCCTCTTTTTCGCAAGTCTCTGCTGGGATGATCAGCTCCTCAACCTCTGCGCTCTTAGT 1024
Db 433 AGCGAGTCTTTTAAAGACATATCCATCGGGGTGTCGCTGTTTACACTGACCGCCCTTTC 492

Qy 1025 GTGACAGTACAGACAGTTCCTCTGAGTGTGTTTCAGGAATTTGGGATTTCTCTTTC 1084
Db 493 GCGAGCGTACTGCGCCATTTGA-----AATCCCTACGCAAGCTTCAGACCAAGCCG 546

Qy 1085 GTAACCTGCATTTGAAATTTGCTCTCCATCTGATCTCTCTTTATCTGCGCCATTTCTGAA 1144
Db 547 CTCACGTCTTTTACTGCGGTGATGATCTGGATCTGCGCATCTTACTGGGCGATGCTTCG 606

Qy 1145 GCGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1169
Db 607 GTTCTTTTCTCGACATCAAGTCT 631

RESULT 13
US-09-960-352-6528
; Sequence 6528, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 2001-09-24
; SEQ ID NO 6528
; LENGTH: 414

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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 28-LIB3058-032-Q1-K1-G11
US-09-960-352-6528

Query Match      1.28; Score 49.6; DB 10; Length 414;
Best Local Similarity 48.6%; Pred. No. 0.026;
Matches 136; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 2359 AATTAGATTAGTATTTTCCACGCTACTATTATTTTAAACACAAATCTTAAGCTA 2418
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 ATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 183
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2419 CAACAAATACACAGGCCCTTAAAGCAGCAGCTGATGACACATTTGGCAGTTTATAGAT 2478
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 243
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2479 GTTACTCAAGAAATTTTAAAGAACTGTATTTATTTTAAAGGCTTTTATTTACAG 2538
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 303
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

2539 GGACCTTGAACATGTTTGTATGTATAATTCAAAGTAATGCTTCAATCAGATAGTCTT 2598
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304 ATATATATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 363
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2599 TTTCAAGTTCAATACGTGTTTTCATGTAATTTTGTAT 2638
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 403
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-960-352-11234
; Sequence 11234, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11234
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
09-960-352-11234

Query Match      1.28; Score 48.6; DB 10; Length 419;
Best Local Similarity 46.8%; Pred. No. 0.045;
Matches 185; Conservative 0; Mismatches 209; Indels 1; Gaps 1;

QY 2174 GATTTCTACTTTTAAAGGATTTTGTCCCTTCAGCCAAACACAAATATGGCTCAGG 2233
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 GCITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 83
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2234 TCACATTTTATTTGAATGTTCATTTGGCCAGTATTTTAACTGCATAATAGCCTAACA 2293
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 143
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2294 TGATTATTTGAACATTTTACACATAGTTTGAAAAAAGACAAAAAATAGTATTCAGG 2353
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAA 203
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2354 TGACCAATTAGATTAGTATTTTCCACGCTCACTATTTATTTTAAACACAAATTTCTAA 2413
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 AGTTAAATTTATTAATTTTAAATTAATAAAAAAATTTTTTTATATATTTTATTA 263
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 2414 AGCTACAACAAATACTACAGGCCCTTAAAGCAGCTGATGACACATTTGGCAGTTTAA 2473
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 264 AATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA-ATAAATAATAAAT 322
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2474 TAGATGTTTACTCAAGAATTTTAAAGAACTGTATTTTAAATGGTGGTTTATTT 2533
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 AAAAAATTTTAAAAAAAATTTTAAAAAAATTTTAAAAAAATTTTATATAAATAATAAAT 382
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2534 ACAAGGGACCTTGAACATGCTTTTGTATGTAAATTT 2568
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 AATTTTATTTTAAATATATATTTTAAATTT 417
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-761-962-2
; Sequence 2, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice
; TITLE OF INVENTION: Variants of Mu-
; FILE OF INVENTION: opiod Receptor (MOR-1) Gene
; CURRENT APPLICATION NUMBER: US/09/761,962
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-2

Query Match      1.18; Score 46.8; DB 10; Length 1238;
Best Local Similarity 51.4%; Pred. No. 0.23;
Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 940 CTTTGGCGTATTTCTTTCAGCTCTTCCCTTTTTCGAGAAGTCTCGTGGGGATCAC 999
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CTTTGGAAACATCCCTCTCGAAGATCGTGATCTCAATAGACTACTACACATGTTCACAG 361
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1000 CGTCTCAACCTCTGCGCTCTTAGTGTTCACAGGTACAGAGCAGTTGCCTCCTGGAGTCG 1059
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TATCTTCACCTCTGACCAATGAGTGTAGACCGCTACATTGCGCTGCCACCCGTCAC 421
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1060 TGTTCAGGAATTTGGGATTCCTTTTGTAACTGCCCATTTGAAATTTGCTCCTCATCTGGATCCT 1119
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 GGCCTGGGATTTCCGTACCCCGGAAATGCCAAATTTGTCAATGTCTGCAACTGGATCCT 481
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1120 GTCCTTTATCTGGCCATTCTCCTGAAGCGAT 1149
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CTCCTCTGCCAATTTGCTGCGCCGTAATGTT 511
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: December 12, 2002, 14:31:28
Job time : 211 secs
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:59:17 ; Search time 141 Seconds
(without alignments)
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Title: US-09-931-157-1

Perfect score: 4105

Sequence: 1 gaattcgccgcctctt.....taaaagttacagaacctt 4105.

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4105	100.0	4105	4	US-08-121-446-1
2	406.2	9.9	1321	4	US-09-175-658B-20
3	395.8	9.6	1873	4	US-08-910-864-13
4	395.8	9.6	4301	4	US-08-121-446-3
5	101.8	2.5	1700	5	PCT-US92-02091-1
6	91	2.2	1726	5	PCT-US92-02091-3
7	79.6	1.9	1205	3	US-09-120-772-1
8	68.6	1.7	1352	5	PCT-US92-02091-7
9	65.8	1.6	1584	5	PCT-US92-02091-5
10	63.6	1.5	1563	1	US-08-279-590A-1
11	63.6	1.5	1563	1	US-08-910-092-1
12	51.4	1.3	3095	6	5231168-1
13	46.8	1.1	1981	4	US-08-387-707-15
14	46.8	1.1	1981	4	US-08-405-271A-15
15	46.2	1.1	595	1	US-08-784-289-1
16	46	1.1	2563	2	US-08-553-436A-7
17	45.8	1.1	19124	2	US-08-487-826B-13
18	44.8	1.1	1443	3	US-08-959-381A-3
19	44.8	1.1	1626	3	US-08-959-381A-4
20	44.2	1.1	1610	3	US-08-889-108-7
21	44.2	1.1	1610	5	PCT-US94-10358-7
22	44.2	1.1	2160	4	US-08-188-275A-1
23	44.2	1.1	2162	4	US-09-351-198-1
24	44.2	1.1	2162	4	US-09-113-426-1
25	44.2	1.1	4156	1	US-08-465-687A-1
26	44.2	1.1	4156	3	US-09-030-970-1
27	44.2	1.1	4156	5	PCT-US94-11843-1

28	43.6	1.1	1422	1	US-08-319-704-5	Sequence 5, Appli
29	43.6	1.1	8700	2	US-08-392-625-16	Sequence 16, Appl
30	43.6	1.1	8700	2	US-08-466-961A-16	Sequence 16, Appl
31	43.6	1.1	8700	2	US-08-645-193B-18	Sequence 18, Appl
32	43.4	1.1	1850	3	US-08-617-860B-32	Sequence 32, Appl
33	43.4	1.1	2570	2	US-09-056-075-2	Sequence 2, Appli
34	43.4	1.1	4098	1	US-08-605-106-4	Sequence 4, Appli
35	43.4	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
36	43.2	1.1	1080	2	US-08-103-170-3	Sequence 3, Appli
37	43.2	1.1	1419	2	US-08-103-170-5	Sequence 5, Appli
38	43	1.0	1080	3	US-08-602-809-3	Sequence 3, Appli
39	43	1.0	1080	5	PCT-US95-16472-3	Sequence 3, Appli
40	42.4	1.0	6124	4	US-08-213-419B-3	Sequence 3, Appli
41	42	1.0	665	2	US-08-883-798A-36	Sequence 36, Appl
42	42	1.0	20674	4	US-09-641-638-651	Sequence 651, App
43	41.8	1.0	5852	1	US-07-867-106-2	Sequence 2, Appli
44	41.6	1.0	20674	4	US-09-641-638-651	Sequence 651, App
45	41.2	1.0	2463	1	US-08-370-542-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-121-446-1
; Sequence 1, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUWA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

Query Match	100.0 %;	Score 4105;	DB 4;	Length 4105;
Best Local Similarity	100.0 %;	Pred. No. 0;		
Matches 4105;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	GAATTGGCGGCGCGCTCTTTCGGGTGCCAGAGTGGAGCTGGAAGTCTGGAGCTTTGGGAGG	60		
1	GAATTGGCGGCGCGCTCTTTCGGGTGCCAGAGTGGAGTGGAGGTCTGGAGCTTTGGGAGG	60		
61	AGACGGGAGACAGACTGGAGCGGTGTCTCCCGAGTGTTCCTCCGAGTGTTCCTTCGTGCGAGCCCT	120		
61	AGACGGGAGACAGACTGGAGCGGTGTCTCCCGAGTGTTCCTCCGAGTGTTCCTTCGTGCGAGCCCT	120		
121	CGCGGCGGTACAGTCAATCCCGTGTGACGATGTGGAGAGCGGTGGAGAGCGCTT	180		
121	CGCGGCGGTACAGTCAATCCCGTGTGACGATGTGGAGAGCGGTGGAGAGCGCTT	180		
181	CATCATATCCACCGGTGTCGCGGGGGATTTGGGTGCCAGCGACACCTCCCGGGAGAA	240		
181	CATCATATCCACCGGTGTCGCGGGGGATTTGGGTGCCAGCGACACCTCCCGGGAGAA	240		
241	CGATGCCAGGAAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAAGCGCCGCCGCGC	300		
241	CGATGCCAGGAAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAAGCGCCGCCGCGC	300		
301	CGGAGCCGGGACACCGCCACCCCTCCGCGCCACCCACCCCTCGCTTCTCGGGCTTCCTC	360		
301	CGGAGCCGGGACACCGCCACCCCTCCGCGCCACCCACCCCTCGCTTCTCGGGCTTCCTC	360		
361	TGGCCCAAGGCGCGCGGACCGCGCAGCTGTCTGCGACGCGGAGCTTCACGCTGAAAA	420		
361	TGGCCCAAGGCGCGCGGACCGCGCAGCTGTCTGCGACGCGGAGCTTCACGCTGAAAA	420		
421	AAAAAGTGAAGGTGTAAAGCAGCAGAGTGCATTAAGAGATATTTCCTCAAAATTCGCT	480		
421	AAAAAGTGAAGGTGTAAAGCAGCAGAGTGCATTAAGAGATATTTCCTCAAAATTCGCT	480		
481	CAAGATGGAACCCCTTTGGCTCAGGCGATCTCTTTGGCTGGCAGCTGTGATCTGTAAAT	540		
481	CAAGATGGAACCCCTTTGGCTCAGGCGATCTCTTTGGCTGGCAGCTGTGATCTGTAAAT	540		
541	CAGTGATAATCCTGAGAGATACAGCAACAATCTAAGCAATCATGTGATGATTTACCCAC	600		
541	CAGTGATAATCCTGAGAGATACAGCAACAATCTAAGCAATCATGTGATGATTTACCCAC	600		
601	TTTTCTGGGCACAGACTCAGCTTCCTGGTTACACCTCATCAACCCATAATTTGGTGCCT	660		
601	TTTTCTGGGCACAGACTCAGCTTCCTGGTTACCACTCATCAACCCATAATTTGGTGCCT	660		
661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGAGACTAAATTTACTTCAGCTTT	720		
661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGAGACTAAATTTACTTCAGCTTT	720		
721	CAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGTTGGGAATGC	780		
721	CAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGTTGGGAATGC	780		
781	AACCTCTCCTCAGAGATCATTTACAGAAACAAATGTATAGGAATGGCCCCAACGCGCTGAT	840		
781	AACCTCTCCTCAGAGATCATTTACAGAAACAAATGTATAGGAATGGCCCCAACGCGCTGAT	840		
841	AGCCAGTCTTGCCTTTGGAGACCTTATCTATCTGTGCTCATTTGATCTCCCTATCAATGATT	900		
841	AGCCAGTCTTGCCTTTGGAGACCTTATCTATCTGTGCTCATTTGATCTCCCTATCAATGATT	900		
901	TAAAGTCTGGCTGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960		
901	TAAAGTCTGGCTGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960		
961	GCCTGTCCCTTTTTCGAAAGTCTCGTGGGGGATCACCGTCTCAACCTCTCGCGCTCT	1020		
961	GCCTGTCCCTTTTTCGAAAGTCTCGTGGGGGATCACCGTCTCAACCTCTCGCGCTCT	1020		

QY	1021	TACTGTTGACAGGTACAGACAGCTTGCCTCTCGAGTCTGTTCACGGAAATTTGGGATTC	1081
DB	1021	TAGTGTGTGACAGGTACAGACAGCTTGCCTCTCGAGTCTGTTCACGGAAATTTGGGATTC	1080
QY	1081	TTTGGTAACTGCCATTGAAATTCCTCCATCTCGATCCCTCTTATCTCTGCGCATTC	1140
DB	1081	TTTGGTAACTGCCATTGAAATTCCTCCATCTCGATCCCTCTTATCTCTGCGCATTC	1140
QY	1141	TGAAGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
DB	1141	TGAAGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
QY	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAAGACTGGTGGCT	1260
DB	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAAGACTGGTGGCT	1260
QY	1261	CTTGGGTTCTATTTCTGTATGCCCTTGGTGTGCATCGGATCTTCTACACCCTCATGAC	1320
DB	1261	CTTGGGTTCTATTTCTGTATGCCCTTGGTGTGCATCGGATCTTCTACACCCTCATGAC	1320
QY	1321	TTTGAGAGTGTGAACAGAGAAGAAATGGCAGCTTGAGAATTCGCCCTCAGTGAACATCTTAA	1380
DB	1321	TTTGAGAGTGTGAACAGAGAAGAAATGGCAGCTTGAGAATTCGCCCTCAGTGAACATCTTAA	1380
QY	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTGTAAATTTTGCCTTTGCTG	1440
DB	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTGTAAATTTTGCCTTTGCTG	1440
QY	1441	CTTCCCTCTTCACCTTAAGCCGTATATTGAAGAAACCTGTGTATACGAAATGACACAGAA	1500
DB	1441	CTTCCCTCTTCACCTTAAGCCGTATATTGAAGAAACCTGTGTATACGAAATGACACAGAA	1500
QY	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTTACATCGGTATTAACCTTGGCAAC	1560
DB	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTTACATCGGTATTAACCTTGGCAAC	1560
QY	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGACGAAGAAATTTAAAAATTG	1620
DB	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGACGAAGAAATTTAAAAATTG	1620
QY	1621	TTTCAGTCTACGCTCTGCTGCTGCTGTTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
DB	1621	TTTCAGTCTACGCTCTGCTGCTGCTGTTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
QY	1681	CATGAACGGAAACAGCATCCAGTGGGAAGAACACAGCATCAAAACACCAACACAGACCG	1740
DB	1681	CATGAACGGAAACAGCATCCAGTGGGAAGAACACAGCATCAAAACACCAACACAGACCG	1740
QY	1741	GAGCAGCCATAAGGACAGCATGAACCTGACCCCTTTAGAAGCACCTCCTCGGTACTCCCAT	1800
DB	1741	GAGCAGCCATAAGGACAGCATGAACCTGACCCCTTTAGAAGCACCTCCTCGGTACTCCCAT	1800
QY	1801	AATCCTCTCGGAGAAAAAATCACAGGCACTGTGACTCCGGGAATCTTCTCTGTATC	1860
DB	1801	AATCCTCTCGGAGAAAAAATCACAGGCACTGTGACTCCGGGAATCTTCTCTGTATC	1860
QY	1861	CTTCTCTCTTAATTCACCTCCACACCCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
DB	1861	CTTCTCTCTTAATTCACCTCCACACCCCAAGAAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
QY	1921	CTGGTTTATCCACCACACATCTACGAATCGTACTTCTTTAATGTATCTAAATTTACATA	1980
DB	1921	CTGGTTTATCCACCACACATCTACGAATCGTACTTCTTTAATGTATCTAAATTTACATA	1980
QY	1981	TTCTCGGTGTTGATTTCAGCACTAAAAATGTTGGAGCTGGGGGAGAAATGAAGACTGTT	2040
DB	1981	TTCTCGGTGTTGATTTCAGCACTAAAAATGTTGGAGCTGGGGGAGAAATGAAGACTGTT	2040
QY	2041	AAATCAAAACCGAAGGATTTACTTCTTCATCAAAATAGAGCTTTTCAAGTACATG	2100
DB	2041	AAATCAAAACCGAAGGATTTACTTCTTCATCAAAATAGAGCTTTTCAAGTACATG	2100
QY	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTTCAATGGGAACCTGGTCACCATGAACCTTAG	2160

; CURRENT APPLICATION NUMBER: US/09/175,658B
 ; CURRENT FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/062,562
 ; PRIOR FILING DATE: 1997-10-21
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 1321
 ; TYPE: DNA
 ; ORGANISM: Horse
 ; US-09-175-658B-20

Query Match 9.9%; Score 406.2; DB 4; Length 1321;
 Best Local Similarity 67.2%; Pred. No. 1.6e-95;
 Matches 630; Conservative 0; Mismatches 283; Indels 24; Gaps 3;

QY 717 CTTTCAATACATTAACACTGTCATATCTGTACTATTTTTCATCGTGGGAATGGTGGGA 776
 Db 310 CTTTCAAGTACATCAACAGTAGTCTGCTGCTAGTGTGCTGGGATCATCGGAA 369
 QY 777 ATGCAACTGCTCAGGATCAATTTACAGAACAAATGTATGAGGAATGCCCCCAACGCCG 836
 Db 370 ACTCCACACTGCTGAGAATCAATTTACAAGAACAAAGTGCATGCGGACGCCCTAATATCT 429
 QY 837 TGATAGCCAGTCTTGCCCTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATG 896
 Db 430 TGATCCGACGCTGCTCCGAGACCTGCTGCAAAATCATATGACGTGCTCCCATCAATG 489
 QY 897 TATTTAAGCTGCTGCTGGCGCTGCCCTTTTGATCACATGACTTTGGGTATTTCTTT 956
 Db 490 TCTACAGCTGCTGGCTGAGGACTGCC-----CTTGGAGTGCAGATGT 534
 QY 957 GCAAGCTGTCCTCTTTTTCGAGAAGTCTCGTGGGGATCACCGTCCCTCAACCTCTGCG 1016
 Db 535 GTAAGCTGCTGCTTTCATACAGAGGCTCCGCTGGGATCATCTGCTGAGTCTGTGTG 594
 QY 1017 CTTCTAGCTTACAGGTACAGAGAGTGGCCCTCGGAGTCTGTTACAGGGAATGGGA 1076
 Db 595 CTTCTAAGTATGACAGATTCGAGTGTGCTTCTTCTTGGAGGAAATTAAGGAATTCGGG 654
 QY 1077 TTCTTTGTAAGTGCATGAAATGTTCTCCATCTGGATCTGCTTATCTTATCTCGCCA 1136
 Db 655 TTCCAAATGAGACAGAGTAGAATTTTAAATTTGGGTGGTCTCTGTTGCTGGCTG 714
 QY 1137 TTCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1196
 Db 715 TCCCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
 QY 1197 CTTCTATGCTCAATGCCAC-----ATCAAAATTCAGGAGTCTTACCAAGATGTAAAG 1250
 Db 775 TCTGCTGCTTCTATCCCACTCAGAAACAGCCTTCTATGAGTCTTACCAAGATGTAAAG 834
 QY 1251 ACTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1310
 Db 835 ACTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
 QY 1311 CCTCATGCTTCTGAGATGTTGACAGAGAAATGGCAGCTTGAGAAATTCGCCCTCAGTG 1370
 Db 895 CCTGATGACCTGTGAATGTTGAGAAAGAGAGTGCCA---TGCAAAATGCTTTAAAG 951
 QY 1371 AACATCTTAAAGCAGGCTGAGAGTGGGAAACAGTCTTCTGCTGCTGCTGCTGCTGCTG 1430
 Db 952 ATCACTTAAAGCAGAGAGAGGAGTGGGAAACAGTCTTCTGCTGCTGCTGCTGCTGCTG 1011
 QY 1431 CTTCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1490
 Db 1012 CCTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1550
 QY 1491 TGGCAAGAACCGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1550
 Db 1072 ATGATCCCAATAGATGTAATTTTGTAGCTTTTGTGATTTGGACTACATTTGGCATCA 1131
 QY 1551 ACTTGGCAACCATGAATTCATGATATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAAT 1610

Db 1132 ACATGGCCTCCCTGAATTCCTGCAATTAATCAATAGTCTCTATTTGGTGAGCAAGAT 1191
 QY 1611 TTAATAATTTTCCAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1647
 Db 1192 TCATAAACTGCTTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1228

RESULT 3
 US-08-910-864-13
 ; Sequence 13, Application US/08910864
 ; Patent No. 6280931
 ; GENERAL INFORMATION:
 ; APPLICANT: SAKAMOTO, AIJI
 ; APPLICANT: HANAOKA, FUMIO
 ; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A CDNA OF AN EXTREMELY
 ; TITLE OF INVENTION: SMALL QUANTITY
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & RICHARDSON P.C.
 ; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400
 ; CITY: LA JOLLA
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,864
 ; FILING DATE: 13-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 216506/1996
 ; FILING DATE: 16-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAILE, LISA A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07998/017001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-678-5070
 ; TELEFAX: 619-678-5099
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1873 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA to mRNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 231..1556
 ; US-08-910-864-13

Query Match 9.6%; Score 395.8; DB 4; Length 1873;
 Best Local Similarity 65.7%; Pred. No. 9.3e-93;
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

QY 689 TGCCACAGCAGACTAAATTTACTTTCAGCTTTCATAATACATTAACACTGTGATATCTGT 748
 Db 498 TGCCAGAGCCCATCCAGATCAAGGAGACTTTCATAATACATCAACAGGTTGTCTCTGC 557
 QY 749 ACATATTTTCATCGTGGGAATGGTGGGAATGCAACCTGCTCAGGATCATTTACCAAGAC 808
 Db 558 CTTGTGCTGCTGCTGGGATCATCGGGAACCTCCACACTTCTGAGAAATATATCAAGAAC 617
 QY 809 AATGTATGAGGAATGGCCCAACGCTGATAGCCAGTCTTGGCCCTTGGAGACCTTATC 868
 Db 618 AAGTGTATCGAAGCGTCCCAATATCTTTGATCGCAGCTTGGCTGGGAGACCTGCTG 677
 QY 869 TATGTGCTATTCCTCTCCCTATCAATGATTTTAAAGTGTGCTGGCGCTGCTGCTTTT 928

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Db 678 CACATCGTCATTGACATCCCTATCAATGCTCTACAGCTGCTGGCAGAGACTGGCC----- 733
QY 929 GATCACAATGACATTTGGCGTATTTCTTTGCAAGCTGTTCCCTCTTTTTCAGAAGTCCCTCG 988
Db 734 -----ATTGGAGCTGAGATGTGTAAGCTGGTCCCTTCATACAGAAAGCCCTCC 782
QY 989 GTGGGATACACGCTCAACCTCTGGCTCTTAGTGTGACAGGTACAGAGCAATGTCCTCC 1048
Db 783 GTGGGAATCACTGCTGCTGAGTCTATGCTCTGAGATTGACAGATATGAGCTGTTGCT 842
QY 1049 TCTGGAGTCTGCTGCTGAGGAATGGAATGCTTTGTTAACTGCAATGGAATGTCCTCC 1108
Db 843 TCTTGGAGTAGAATTAAGGAATTTGGGTTTCCAAATAGGACAGCAGTAGAATGCTTTG 902
QY 1109 ATCTGGATCTGCTCTTTATCTCTGGCATCTCTCAAGCGATTGCTGCTGATGTCACCC 1168
Db 903 ATTTGGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
QY 1169 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 963 ATGGACTACAAAGGAAGTTATCTCGAATCTGCTTGTCTTCATCCGTTTCAGAAGCAGCT 1022
QY 1223 TTTATGCACTTACCAAGATGTAAGAGCTGTTGGCTCTTTCCGGTCTATTTCTGTATG 1282
Db 1023 TTTATGCACTTACCAAGAGCAAGAAAGATTGGTGGCTATTTCAGTTTCTATTCTGCTTG 1082
QY 1283 CCCTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342
Db 1083 CCATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
QY 1343 AATGGCAGCTTGAAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1402
Db 1140 AATGGTGGCATGAGATGCTTTAAATGATCACCATAAGCAGACAGCGGAGTGGCCAAA 1199
QY 1403 ACAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462
Db 1200 ACCGCTCTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1259
QY 1463 ATATTGAAGAAACTGTATATACGAATATGGAAGTGAAGCAAGCAAGTGAATGTAATG 1522
Db 1260 ATTTCAAGCTCACTCTTTAATATCAAGAAATGATCCCAATAGATGTAACATTTTGA 1319
QY 1523 TTAAGTCTGATGATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1582
Db 1320 CTGTTGGTATGCACTATATGTTATCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
QY 1583 ATAGCTCTGATTTTGTGAGCAAGAAATTTTAAATTTTCCAGTCAATGCTGCTGCTG 1642
Db 1380 ATGCTCTGATTTTGTGAGCAAGAAATTTTAAATTTTCCAGTCAATGCTGCTGCTGCT 1439
QY 1643 TGCTG 1647
Db 1440 TGCTG 1444

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RESULT 4

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US-08-121-446-3
; Sequence 3, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUHA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566
; US-08-121-446-3

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Query Match 9.68; Score 395.8; DB 4; Length 4301;
Best Local Similarity 65.7%; Pred. No. 1.4e-92;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

QY 689 TGCCACAGCAGACTAAATTTACTTACAGCTTTCAATATACATTAACACTGTGATATCTCT 748
Db 505 TGCCAGGACCCATCGAGATCAAGAGACTTTCAATATACATCAACACGGTTGTGCTCTC 564
QY 749 ACTATTTTCATCGTGGGAATGGTGGGAATCAACTGCTCAGGATCATTTTACCAGAAC 808
Db 565 CTTGTGTTGCTGCTGGGATCATCGGAACTCCACACTTCTGAGAATTTATCTACAAGAAC 624
QY 809 AAATGATAGGAATGGCCCAACGCGTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
Db 625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
QY 869 TATGTGTCATTGATCTCCCTATCAATGATTTTAAAGCTGCTGGCGTGGCGCTTTT 928
Db 685 CACATGCTGATGATCCCTATCAATGCTCAAGCTGCTGGCAGAGACTGGCC----- 740
QY 929 GATCACAATGACTTTGGCGTATTTCTTTTSCAAGCTGTTTCCCTTTTTCAGAAAGTCTCC 988
Db 741 -----ATTTGGAGCTGAGATGTGTAAGCTGCTGCTTTTCATACAGAAAGCTCC 789
QY 989 GTGGGATACCCGCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAATGTCCT 1048
Db 790 GTGGGAATCACTGCTGCTGAGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
QY 1049 TCCGTGGAGTCTGTTTCAGGGAATGGGATTCCTTTGGTAACTGCCATTTCAAAATGCTCTCC 1108
Db 850 TCTTGGAGTAGAATTAAGGAATTTGGGTTTCCAAATAGGACAGCAGTAGAATTTGTTG 909
QY 1109 ATCTGGATCTGCTCTTTTATCTCTGCGCATTTCTGAAGGATTTGGCTTCTGCTCATGTCCT 1168
Db 910 ATTTGGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 1169 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1029
QY 1223 TTTATGCACTTACCAAGATGTAAGAGCTGTTGGGCTCTTCCGGTCTCTATTCTGTATG 1282

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Db 1030 TTCAAGCAGTTTACAGACAGCAAAAGATTGGTGGCTGTTTCAGTCTTCTATTTCTGCTTG 1089
QY 1283 CCCTTGTGTGCACTGGGATCTTACACCCCTCATGCTTGTGAGATGTTGAACAGAGG 1342
Db 1090 CCATTGCCATCACTGCATTTTATACACTAATGACCTGTGAATGTTG--AGAAAG 1146
QY 1343 AATGGCAGCTTGAAATGCGCTCAGTGAACATCTTAAGCAGCCTGAGAAAGTGGCAAAA 1402
Db 1147 AAAAGTGGCATGCAATGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCAAAA 1206
QY 1403 ACAGTTTCTGCTGGTGTGAATTTTGGCTTTGCTTGGTGGTTCCTCTCTCACTTAAAGCGT 1462
Db 1207 ACCGCTCTTTTGGCTGGCTGCTTGTCTTGGCTCTGCTGGCTTCCCTTCACCTCAGCAGG 1266
QY 1463 ATATTGAAGAAACCTGTGTATAGCAAAATGACAAAGACCAAGCATGTGAATTAATTTAGTTTC 1522
Db 1267 ATCTGAAGCTCACTCTTTATATACAGATGATCCCAATAGATGACATTTTGAAGCTTT 1326
QY 1523 TTACTGCTCATGGAATACATCGGTATTAACTTTGCAACCAACCATGAATTCATGATTAACCC 1582
Db 1327 CTGTTGTTATGGACTATATTGTTATCAACATGGCTTCACTGAATTCCTGCAATTAACCCA 1386
1583 ATAGCTCTGATTGTTGACCAAGAAATTTAAATTTGTTTCCAGTCATGCTCTGCTGC 1642
Db 1387 ATTGCTCTGATTGTTGGTGAGCAAAAGATTCAAAACTGCTTTAAAGTCATGCTTATGCTGC 1446
QY 1643 TGCTG 1647
Db 1447 TGGTG 1451

RESULT 5

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02091

; FILING DATE: 19920313

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/426,150

; FILING DATE: 24-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/533,659

; FILING DATE: 05-JUN-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34090

; REFERENCE/DOCKET NUMBER: A-0092C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-266-7476

; TELEFAX: 415-266-7400

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1700 base pairs

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; APPLICANT: Harkins, Richard N.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Battey Jr., James F.

; GENERAL INFORMATION:

; Sequence 3, Application PC/TUS9202091

; PCT-US92-02091-3

; RESULT 6

; PCT-US92-02091-3

; Sequence 3, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

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QY	720	TCAAATACATTTAACACTGTGATATCTTGTACATATTTTCATCGTGGGAATGTGGGGAATG	779
Db	514	TCCTCTATGTCACTCCCTCGAGTTTATGGGGTTATCATTTCTGATAGCGCTCATTTGGCAACA	573
QY	780	CAACTCTGCTCAGGATCACTTTACCAGACAAATGATCAGGAATGGCCCCAACCGCGTGA	839
Db	574	TCACCTTTGATCAGATCTCTGTACAGTCAAGTCCATCGGAAACGTTCCAAACCTGTTCA	633
QY	840	TAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCACTATGAT	899
Db	634	TTTCCAGTCTGCGCTTTGGGAGACCTGCTCCTCTAATAACGTGCTCCAGTGGATGCCA	693
QY	900	TTAAGCTGCTGCTGGCGCTGCGCTTTTGTATCACAATGACTTTGGCGGTATTTCTTTTGA	959
Db	694	GCAGGTACTGCGCTGACAGATGCGCTATTTGGCAGGATTTGGC-----TGA	738
QY	960	AGCTGTTCCTCTTTTGGCAAGTCTCGGTGGGGATCACCGTCTCAACCTCTGCGCTC	1019
Db	739	AACTGATCCCTTTATACAGCTTACTCTGTGTGGGTCTGTCTTCCACTCAACGCGC	798

Best Local Similarity 46.9%; Pred. No. 6.8e-11;
Matches 419; Conservative 0; Mismatches 439; Indels 36; Gaps 4;

QY	761	GTGGCAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAACAATGTATGAGG	820
Db	180	GTGGGATCCCTTGGAAATGCTATTCTCATCAAGTCTTTTTCAGAGCCAAATCCCATGAA	239
QY	821	AATGCCCCAAACGCGCTGATAGCCAGTCTTGCCCTGGAGACCTTATCTATGTGTGTCATT	880
Db	240	ACAGTTCAAATATTTTCATCACCAGCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT	299
QY	881	GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGCGCTTGCCCTTTTTCATCACAATGAC	940
Db	300	TGTTGGCCAGTGGATGGCAACTCACTFACCTTGCAGAAGGATGCGTGTTC-----	347
QY	941	TTTGGCGTATTTCTTTCGAAGTGTTCCTCTTTTTCGAGAAGTCTCCGGTGGGATCAC	1000
Db	348	--GGAAGAATTTGGTTGTAAGTGCTCTCTTTTCATCCGGCTCACCTTCCTGTGGTGTC	404
QY	1001	GTCTCTCAACCTCTGCGCTTAGTCTTCACAGGTACACAGCAGTTCCTCTGGAGTCGT	1060
QY	405	GTGTTTCATTAGCAATTTCTCAGCGCTGACAGATACAAGCGAGTTGTGAAGCCACTTGAG	464
QY	1061	GTTCCGGAATTTGGGATTCCTTTGGTAATGCTGCATTTGAATTTGCTCCACTCTGGATCCTG	1120
Db	465	CGACAGCCCTCAATGCCATCCTGAAGACTGTGTAAAGCTGGCTGGGTGATGCTG	524
QY	1121	TCCTTTATPCCTGGCCATTCCTGAAGCGAATTTGGCTTCGTCATGGTACCCCTTTGAATATAGG	1180
Db	525	TCTATGATATTTGCTCTACCTGAGGCTATATTTCAATGTATACACTTTTCGAGATCCC	584
QY	1181	GGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTGTACCAA	1240
Db	585	AATAAAAATATGACATTTTGAATCATGTACCTCTATCTCTCTCTAAGAAGCTCTTGCAA	644
QY	1241	GATGTAAGGACTGCTGGCTCTTCGGGTCTATTTCTGTATGCCCTTGGTGTGCACTGCG	1300
-Db	645	GAATACATTTCTGCTGTGCTCTTATAGTGTCTACATTTATCCACTCTCTATTATCTCT	704
QY	1301	ATCTTCTACACCCCTCATGACTTTGTGAGATGTTGAACAGAGAAGAAATGGCAGCTTGAGAAT	1360
Db	705	GTCTACTATTCTTGATTTAGGACCTTTTACAAAGCACCCGTGAACATACCTTACTGAG	764
QY	1361	GCCCTGAGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAACAGTTTTTC	1411
Db	765	GAACAAAGCCCATGCCGTGAAGCAGATTTGAATCCCGAAAGAGAATTTGCCAGAACGGTAT	824
QY	1412	TGCTTGGTTGTAATTTTGGCTCTTTTGGTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG	1471
-Db	825	GTGTTGGTGGCTCTGTTTGGCCCTCTGCTGGTTGGCAATACCT--CCTGTACCTCTACC	882
QY	1472	AAAACTGTGTATAAGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC	1531
Db	883	ATTCAATTCACCTTCTCAAAACCTATGTAGACCCCTCTGCCATGCATTTCAATTTCCACAT	941
QY	1532	ATGATTACATCGGTATTTAACTTTGGCAACCATGAATTCATGTATAAAACCCCATAGCTCTG	1591
Db	942	-----TTCTCTCGGGTTTTGGCTTTCAGCAATCTTCGGTAAACCCCTTTCCTCTC	992
QY	1592	TATTTTGTGACAAAGAAATTTAAAAATTTGTTTTCAGTCATGCCCTCTGCTGCTGC	1645
Db	993	TACTGGCTGACAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC	1046

RESULT 8

PCT-US92-02091-7

PC1 0392 02091 /
; Sequence 7, Application PC/TUS9202091

; GENERAL INFORMATION:

APPLICANT: Battey Jr., James F.

APPLICANT: Corjay, Martha H.

APPLICANT: Feldman, Richard I.

APPLICANT: Harkins, Richard N.

;
;
;
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwin P. Ching
STREET: 1501 Harbor Bay Parkway
CITY: Alameda
STATE: CA
COUNTRY: USA
ZIP: 94501
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02091
FILING DATE: 19920313
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/426,150
FILING DATE: 24-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/533,659
FILING DATE: 05-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34090
REFERENCE/DOCKET NUMBER: A-0092C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-266-7476
TELEFAX: 415-266-7400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1352 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Small cell lung carcinoma
CELL LINE: NCI-H345
FEATURE:
NAME/KEY: CDS
LOCATION: 140..1312
PCT-US92-02091-7

Query Match 1.7%; Score 68.6; DB 5; Length 1352;

Query Match 1.7%; Score 68.6; DB 5; Length 1352;
Best Local Similarity 50.1%; Pred. No. 5.1e-08;
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

Qy	752	ATTTTCATCTGCGGAATGGTGGGGAATGCAAC	TCTGCTCAGGATCATTTACAGAACAA	811
Db	296	ATCATCACCCTGGGCTGTCTGGCAACATCAT	CTGGTGAAGATCTTCATCACCAACAGC	355
Qy	812	TGATATGAGGAATGGCCCCAACGCGCTGATG	CCAGCTTTGGCCCTTGGAGACCTTATCAT	871
Db	356	GCCATGAGGAGCGTCCCAACATCTTCATCT	CTAACTCGCGCGCGGAGCTTGTGCTG	415
Qy	872	GTGCTCATTTGATCTCCCTATCAATGATTTA	AGCTGCTGGCTGGGCGCTGGCCTTTTGAT	931
Db	416	CTGCTCACCTCGCTCC-----GGTGCAGC	CTCGGCTACTTCTTCGAC	460
Qy	932	CACAATGACCTTTGGCGTATTTCTTTGCAAG	CTGTCCCTTTTTTGCAAGTCTCTGGG	991
Db	461	GAGTGGATGTTTGGCAAGGTGGGCTGCAAA	TGATCCCTGTCTATCCAGCTCACTTCCG	520
Qy	992	GGGATCACCGTCTCAACCTCTCGGCTCTTA	GTGTTGACAGGTACAGACGAGTGGCTCC	1051
Db	521	GGGGTTTCCGTGTTCACTCTCACTGCGCTC	ACGCGGACAGAGTACAGACCCATCGTTAA	580
Qy	1052	TGGAGTCTGTTTCAGGGAATTGGGATTCCT	TTGGTAACCTGCCATTGCTCTCCATC	1111

Db	581	CCCATGGACATGCAGACGTGCGGGCATTCCTGGCACCTGTCTGAAGGCCATCGGTATC	640
Qy	1112	TGGAATCCTGTCCTTTATCCTGGCCATTCCTGAACGATTGGCTTCGTCATGGTACCCCTT	1170
Db	641	TGGGTGTCCTCCGTGTGCTGGCAGTTTCCGACGCGGTGTTTTCAGAAATGGCTCGCAT	699

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RESULT 9
PCT-US92-02091-5
; Sequence 5, Application PC/TUS9202091
; GENERAL INFORMATION:
; APPLICANT: Bartey Jr., James F.
; APPLICANT: Corjay, Martha H.
; APPLICANT: Feidman, Richard I.
; APPLICANT: Harkins, Richard N.
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwin P. Ching
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02091
FILING DATE: 19920313
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,150
FILING DATE: 24-OCT-1989
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TELECOMMUNICATION INFORMATION:
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Query Match 1.6%; Score 65.8; DB 5; Length 1584;
Best Local Similarity 49.6%; Pred. NO. 3e-07;
Matches 209; Conservative 0; Mismatches 197; Indels 15; Gaps 1;

QY	752	ATTTTCATCGTGGGAATGCTGGGGAATGCAACTCTGCTCAGGATCATTTACCAACAATAA	811
Db	288	ATCATCTCGGTGGGCTTGCTGGCAACATCATCTGGTAGAATATTCCACCAACAGC	347
QY	812	TGTATCAGGAATGCCGCCAACGCCTGTAGCACGTCTTGCCCTTGGAGACCTTAATCAT	871
Db	348	ACCATCGGAGTGTCCCCAAACATCTTCATCTCTAACCTGGCTGCGGAGACCTGCTGTG	407

Qy	872	GTGTCATATGATCTCCCTCAATCAATGATTTAAAGCTGCTGGCTGGCGCTGGCCCTTTTGAT	931
Db	408	CTGCTGACCTGCGTCCCGAGTGGATGCTCC-----CGATACTTCTTTGAT	452
Qy	932	CACAAAGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTCTTTTTCGAGAAGTCTCTCGGTG	991
Db	453	GAATGGGTGTTGGGCAAGCTGGGCTGCAAACTCATCCAGCCATCCAGTCACTCACCTCGGTG	512
Qy	992	GGATCACCGTCTCAACCTCTCGCTCTTACTGTTGACAGTACAGAGCAGTTCGCCTCC	1051
Db	513	GGGGTTTCGTGTTCACTCTCACGGCCCTCAGCGCTGACAGGTACAGAGCTATCGTGAAC	572
Qy	1052	TGGAGTCGTCTTCAGGGAATTGGGATTCCTTTGGTAAGTCGCCATTGAAATGTCTCCATC	1111
Db	573	CCATGGACATGCAGACGTCTGGTGTGGTGTGTGGACCAAGTTTGAAGCCCGTGGGCATC	632
Qy	1112	TGGATCCTGTCCTTTTATCTCGGCCATTCCTGAAGCGATTGGCTCGTCATGATACCCCTTT	1171
Db	633	TGGGTGCTCTCTGCTGTTGGCTGTCCCTGAGGCTGTCTTTTCGGAAGTAGCAGCATC	692
Qy	1172	G 1172	
Db	693	G 693	

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RESULT 10
US-08-279-590A-1
; Sequence 1, Application US/08279590A
; Patent No. 5656749
; GENERAL INFORMATION:
; APPLICANT: ELIOT R. SPINDEL, SRINIVASA
; APPLICANT: NAGALLA AND BRENDA BARRY
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,590A
; FILING DATE: July 22, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5556749e
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Y. Rocky Tsao
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/098001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1563
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-279-590A-1

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Query Match
1.58; Score 63.6; DB 1; Length 1563;

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Best Local Similarity 45.5%; Pred. No. 1.1e-06;
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

QY 735 CTGTGATATCTTGTACTATTTTCATCTGGGAATGGTGGGAATGCAACTCTGCTCAGGA 794
D 735 CTGTGATATCTTGTACTATTTTCATCTGGGAATGGTGGGAATGCAACTCTGCTCAGGA 794
QY 340 CTGTACATATGCTGTTATTTTCGTCGGTATCTTGGAAACAAATCTTATAAAG 399
D 340 CTGTACATATGCTGTTATTTTCGTCGGTATCTTGGAAACAAATCTTATAAAG 399
QY 795 TCATTATACAGACAAATGATGAGAAATGGCCCAAGCGGTGATGAGCAGTCTGGCCC 854
D 795 TCATTATACAGACAAATGATGAGAAATGGCCCAAGCGGTGATGAGCAGTCTGGCCC 854
QY 400 TATTTTAAAAATCAAGTCAATGAGAGTGTTCCTAATATTTTCATCACCAGCTGGCTT 459
D 400 TATTTTAAAAATCAAGTCAATGAGAGTGTTCCTAATATTTTCATCACCAGCTGGCTT 459
QY 855 TTGGAGACCTTATCTATGTTGCTGATGATCTCCCTATCAATGATGATGATGATGATG 914
D 855 TTGGAGACCTTATCTATGTTGCTGATGATCTCCCTATCAATGATGATGATGATGATG 914
QY 460 TTGGAGATCTTCTTCTACTGCTGACCTGCGTGGCAGTGGACGATCTCGGTATATTG 519
D 460 TTGGAGATCTTCTTCTACTGCTGACCTGCGTGGCAGTGGACGATCTCGGTATATTG 519
QY 915 GCGCTGGCTTCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 974
D 915 GCGCTGGCTTCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 974
QY 520 ACACGTGGATGTTTGGAAAGCTGGCTGT- 564
D 520 ACACGTGGATGTTTGGAAAGCTGGCTGT- 564
QY 975 TCAGAAATCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034
D 975 TCAGAAATCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034
QY 565 TACAGCTTACCTCTCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
D 565 TACAGCTTACCTCTCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 1035 ACAGAGCAGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
D 1035 ACAGAGCAGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
QY 625 ACAGAGCAGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
D 625 ACAGAGCAGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
QY 1095 TTGAAATTTCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1154
D 1095 TTGAAATTTCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1154
QY 685 GCAAAGCTGTTTGTGTTGATCATTTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
D 685 GCAAAGCTGTTTGTGTTGATCATTTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
QY 1155 TCGTCATGTCACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
D 1155 TCGTCATGTCACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
QY 745 CAGATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
D 745 CAGATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
QY 1215 CATCAAAATTCATGAGTCTTACCAGATGTAAGAGAGTGGTGGCTCTTCGGGTTCTATT 1274
D 1215 CATCAAAATTCATGAGTCTTACCAGATGTAAGAGAGTGGTGGCTCTTCGGGTTCTATT 1274
QY 805 ATCCAGTCTCTGAAAAGATCTGCAAGAGACACATTCCTTAATATGCTTCCCTGGTATTCT 864
D 805 ATCCAGTCTCTGAAAAGATCTGCAAGAGACACATTCCTTAATATGCTTCCCTGGTATTCT 864
QY 1275 TCTGTATGCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1334
D 1275 TCTGTATGCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1334

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RESULT 11

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US-08-910-092-1
; Sequence 1, Application US/08910092
; Patent No. 5814463
; GENERAL INFORMATION:
; APPLICANT: Spindel, Eliot R.
; APPLICANT: Nagalla, Srinivasa
; APPLICANT: Barry, Brenda
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS
; TITLE OF INVENTION: FOR BOMBESIN-LIKE PEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

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; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,092
; FILING DATE: 12-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,590
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/098002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1563 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 192...1319
; US-08-910-092-1

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Query Match 1.5%; Score 63.6; DB 1; Length 1563;
Best Local Similarity 45.5%; Pred. No. 1.1e-06;
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

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Db 865 ACATTGTTCCCTGTCATCATTTCTGTCATATTTACTTCCCTATTTGCAAAACCCCTGTACA 924
Qy 1335 A-----CAGAAGGAATGGCAGCTTGAGAATTCCTCAGTGAACATCTTAAGCAGC 1385
Db 925 AAGTACTTTCAACATGCTCTGNAGAGCACACACGCCCGGAACAGATAGATCGC 984
Qy 1386 GTCGAGAAGTGGCAAAACAGTTTCTGCTGGTGTGAATTTTGTCTCTTTGCTGGTTCC 1445
Db 985 GCAACAGAGTGGCAAAACAGTTTCTGCTGGTGTGGTGGCATTTGTCGCACTGTCTGGTTGC 1044
Qy 1446 CTCCTCACTT 1455
Db 1045 CAACACCAT 1054

RESULT 12
5231168-1/c
Patent No. 5231168
APPLICANT: DIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
SEQ ID NO: 1:
LENGTH: 3095
5231168-1

Query Match 1.3%; Score 51.4; DB 6; Length 3095;
Best Local Similarity 42.6%; Pred. No. 0.0023;
Matches 335; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

Qy 2151 GAACCTTTAGAGATTAACGACAGATTTCTACTTTTAAAGTGAATTTTGTCCCTTCA 2210
Db 2999 GACATTATAAACTTACTTTTCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATA 2940
Qy 2211 GCCAAACACATATGGCTCAGGTCACCTTTTATTTGAATGTCATTTGGTCCCATTTT 2270
Db 2939 TTTAAATTTAAATAATATATATGAATTTTATACCTTAAGAAATATAATCAGAACATAG 2880
Qy 2271 TTTAACTGCATAATAGCCTAACATGATTTTGAACCTATTATACACATAGTTTGAAAAA 2330
Db 2879 ATTATTGTTTCATATTTTATTCGCAATTTATGCCAAAGGCAACATGATATATATAA 2820
Qy 2331 AAAGACAAAATAGTATTCAGGTCAGCAATTAGATTAATTTTCCAGCTCATTTTAA 2390
Db 2819 TATATACATAAATTTATCCAGTATTTATATATAATAAATTTATTTATATAATTTATGAAA 2760
Qy 2391 TTTTAAACACACAAATTTCTAAAGCTACACAAATTAACAGCCCTTAAGCACAGTC 2450
Db 2759 AAAATGATAATAAAAAATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 2700
Qy 2451 TGATGACACATTTGGCAGTTTAAATAGATTTTACTCAAGAAATTTTAAAGAACTGATTT 2510
Db 2699 TTTCTTAAATAATACATAAATAAATTTTCTTTTATTTATATATAAAGCCAGAAAT 2640
Qy 2511 TATTTTAAATGGTGTGTTTATTAACAAGGACCTTTGACATGTTTGTATGTTAAATTTCA 2570
Db 2639 TTTTATTTATACATGATATACATTTTCAAGTATTAATAAATAATATCTGTAATTTCTATATTTA 2580
Qy 2571 AAAGTAAATGCTTCATACAGATAGTTCTTTTTCACAAAGTTCATTAATTTTCAATGAAA 2630
Db 2579 TTTTATATATTTTATAGAAATTAATAACAACCTAAGAAAAGAAATTTATTTATTTATTTT 2520
Qy 2631 TTTTGTATGAAAATCAATGCAAGTACCAAGTACCAAAATGTTAAATGATGTGTCATTTAACTG 2690
Db 2519 TTTCTAATAATATACATGAATTTATTTCTATATATACAGAAATCCTAGTATTTCTTTA 2460
Qy 2691 CCTGAGACTTTCTAGTGCACGTATATAGAAAGTCTTAAACACACACCTAAGAGAAAAGATCG 2750
Db 2459 TATAATATATATATTTTATTAATAAATAATATTTAGTTACATATATATAAGAAAAAATTTT 2400

Qy 2751 A-----ATTTTCAGATGATTCGAAATTTTTCATTTCAGTATTTGTAAATAGTACATAT 2804
Db 2399 ATTTAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2340
Qy 2805 ATATGATATACATATACCTCTCTATTCCTTAAATTTTGTAAAAATGTTAACTGGCAGT 2864
Db 2339 AAAAAATATACATATATCTTCTGCTATTCCTTAAATTTGTTAACTTGAATAACACCA 2280
Qy 2865 AAGTCTTTTTCATCTCCCTTTCCATATAGGAACACATAATTTGAAGTGGCCAGATG 2924
Db 2279 TCATATGATTAATCATACACTTACATAGTTTGGAGATCTTTTAAATTTCTTTGTA 2220
Qy 2925 AGTTTAT 2931
Db 2219 GATATAT 2213

RESULT 13
US-08-387-707-15
Sequence 15, Application US/08387707
Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,707
FILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-387-707-15

Query Match 1.1%; Score 46.8; DB 4; Length 1981;
Best Local Similarity 51.4%; Pred. No. 0.028;
Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 940 CTTTGGCGCTATTTCTTTCGACAGCTGTTCCCTTTTTCGAGAGAGTCTCGGTGGGATCAC 999
Db 657 CTTTGGAAACATCTCTGCAAGATCGTGATCTCAATAGACTACTACAACATGTTCCACAG 716
Qy 1000 CGTCTCAACCTTCGCGCTCTTAGTGTTCAGAGGTACAGAGCAGTTCCTCTCTGGAGTCG 1059
Db 717 TATCTTCACCTCTGCGACCATGAGTAGCCGCTACATTCGCTGCTGCCACCCGCTCAA 776
Qy 1060 TGTTCAGGAATTTGGGATTTCTTGTAACTGCCATTTGAAATTTGTCTCCATCTGGATCCT 1119
Db 777 GGCCCTGGATTTCCGTACCCCGCCGGAATGCCAAATTTGTCAATGTCTGCAACTGGATCCT 836

QY 1120 GTCTTTATCTGCGCATTCCTGAAGCGAT 1149
 |||||
 Db 837 CTCTTCTGCGCATTCCTGCGCGTAATGTT 866

RESULT 14

US-08-405-271A-15
 ; Sequence 15, Application US/08405271A
 ; Patent No. 6432652
 ; GENERAL INFORMATION:
 ; APPLICANT: EVANS, CHRISTOPHER J.
 ; APPLICANT: KEITH, DUANE E.
 ; TITLE OF INVENTION: OPIOID RECEPTOR GENES
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/405,271A
 FILING DATE: 14-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20526.22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEX: 90-4030 MRSNFOERSWSH
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1981 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-405-271A-15

Query Match 1.1%; Score 46.8; DB 4; Length 1981;
 Best Local Similarity 51.4%; Pred. No. 0.028;
 Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 940 CTTTGGCGTATTCTTTGCAAGCTGTTCCCTTTTGGCAGAGTCTCCGTTGGGATCAC 999
 |||||
 Db 657 CTTTGGAAACATCTCTGCAAGATCGTGATCTCAATAGACTACTACAACATGTTCCACGAG 716
 QY 1000 COTCTCAACCTCTCGGCTCTTGTAGTTGACAGAGTACAGACGAGTTGCCCTCGGAGTCG 1059
 |||||
 Db 717 TATCTTCACCTCTGCACCATGAGTGATAGACCGCTACATTCGCGTCTGCCACCGGTCAA 776
 QY 1060 TCTTCAGGGAATGGGATTCCTTTGGTAACTGCCATTGAAATGTCTCCATCTGGATCCT 1119
 |||||
 Db 777 GGCCCTGGATTTCCGCTACCCGCAAAATGTGCAATGTCTGCAACTGGATCCT 836
 QY 1120 GTCTTTATCTGCGCATTCCTGAAGCGAT 1149
 |||||
 Db 837 CTCTTCTGCGCATTCCTGCGCGTAATGTT 866

RESULT 15

US-08-784-289-1
 ; Sequence 1, Application US/08784289
 ; Patent No. 581912
 ; GENERAL INFORMATION:
 ; APPLICANT: Pedrazzini, Thierry

APPLICANT: Brunner, Hans R
 TITLE OF INVENTION: Transgenic Animals with Disrupted NPY Y1
 TITLE OF INVENTION: Receptor Genes
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Vinson & Elkins L.L.P.
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.
 ZIP: 20004-1008
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/784,289
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Sanzo, Michael A
 REGISTRATION NUMBER: 36,912
 REFERENCE/DOCKET NUMBER: BMR 350/13000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 639-6585
 TELEFAX: (202) 639-6604
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 595 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-784-289-1

Query Match 1.1%; Score 46.2; DB 1; Length 595;
 Best Local Similarity 50.7%; Pred. No. 0.021;
 Matches 111; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 711 CTTACGCTTTCAATACATTAAACACGTGTGATATCTTCTACTATTTCATCTGGGAATGG 770
 |||||
 Db 45 CCTTGGCTGTGATATTACCTTAGCTTGGCTGTGATATTCTTGGGTCT 104
 QY 771 TGGGGAATGCACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCA 830
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 Db 105 CTGGAACCTGGCATTGATCATATCATCTCTAAACACAGAGAGATGAGGAATGTACCA 164
 QY 831 ACGCGTGATAGCCAGCTTGGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTA 890
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 Db 165 ACATTCGTGATCGTGAACCTCTCCTTCTCAGACTTGTCTGTCGCGAGTCATGTCTCCCGT 224
 QY 891 TCAATATATTAAAGCTGTGGCTGGCGCTGGCTTTTG 929
 |||||
 Db 225 TCACCTTTGTGTACACACTGATGGACCACTGGGTCTTCG 263

Search completed: December 12, 2002, 14:28:11
 Job time : 169 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 08:12:06 ; Search time 761 Seconds
(without alignments)
12147.770 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
Sequence: 1 gaattcgccgcctcttg.....taaaagttacagaaacctt 4105

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4103.4	100.0	4105	14	AAQ34583
2	4103	100.0	4105	21	AAQ34583
3	2470	60.2	2595	24	AAQ34583
4	2470	60.2	2595	24	AAQ34583
5	2470	60.2	2595	24	AAQ34583
6	1819.6	44.3	1868	21	AAQ34583
7	1819.6	44.3	1868	21	AAQ34583
8	1819.6	44.3	1868	21	AAQ34583
9	1819.6	44.3	1868	21	AAQ34583

10	1819.6	44.3	2008	21	AAF20904	Human low adenosin
11	1819.6	44.3	2008	21	AAQ34782	Human adenosine re
12	1819.6	44.3	5036	21	AAF21447	Human endothelin r
13	1819.6	44.3	117609	21	AAF21435	Human receptor-rel
14	1296.8	31.6	1310	21	AAF20902	Human endothelin r
15	1296.8	31.6	1310	21	AAF20914	Human ELAM-1 polyn
16	1296.8	31.6	1310	21	AAQ34780	Human adenosine re
17	1296.8	31.6	1310	21	AAQ34782	Human adenosine re
18	1296.8	31.6	146981	21	AAF21442	Human ELAM-1 polyn
19	1280.8	31.2	1284	23	AB197987	Non-endogenous hum
20	1248.8	30.4	1284	23	AAQ32099	Human endothelin r
21	403.8	9.8	1965	13	AAQ25892	Sequence encodes e
22	399	9.7	4301	14	AAQ34584	ETb receptor gene
23	396.6	9.7	1406	15	AAQ53922	Bovine ET receptor
24	395.8	9.6	1632	24	AAQ24966	Human G-protein co
25	395.8	9.6	1719	21	AAF21285	Human low adenosin
26	395.8	9.6	1720	21	AAQ35163	Human adenosine re
27	395.8	9.6	1872	21	AAF21283	Human low adenosin
28	395.8	9.6	1872	21	AAQ35161	Human adenosine re
29	395.8	9.6	1873	19	AAV17875	Homo sapiens endot
30	395.8	9.6	4286	21	AAF21284	Human low adenosin
31	395.8	9.6	4286	21	AAQ35162	Human adenosine re
32	395.8	9.6	13611	21	AAF21288	Human low adenosin
33	395.8	9.6	13612	21	AAQ35166	Human adenosine re
34	392.6	9.6	1329	23	AB197988	Non-endogenous hum
35	383.2	9.3	1958	24	AB199321	Mouse ischaemic co
36	381.2	9.3	1578	21	AAF21287	Human low adenosin
37	381.2	9.3	1578	21	AAQ35165	Human adenosine re
38	343	8.4	343	20	AAH87097	Human single nucle
39	284.4	6.9	438	24	ABL80342	Human ovarian canc
40	256.2	6.2	267	21	AAQ4557	Human secreted pro
41	255	6.2	255	19	AAH11241	Human biallelic po
42	246.4	6.0	9118	24	ABQ66989	Human angiogenesis
43	246.4	6.0	9543	24	ABN80048	Human chemically m
44	243.6	5.9	9118	24	ABQ66990	Human angiogenesis
45	243.6	5.9	9543	24	ABN80049	Human chemically m

ALIGNMENTS

RESULT 1

AAQ34583
ID AAQ34583 standard; DNA; 4105 BP.

XX AAQ34583;

XX 11-MAY-1993 (first entry)

DE Eta receptor gene.

XX Human; ETA; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 485..1768

FT sig_peptide /tag= a

FT mat_peptide 485..544

FT polyA_signal 545..1765

FT misc_feature /tag= c

FT misc_feature 4084..4089

FT misc_feature /tag= d

FT misc_feature /tag= e

FT misc_feature /function= Related with mRNA instability

FT misc_feature 2059..2063

FT misc_feature /tag= f

FT misc_feature /function= Related with mRNA instability

FT misc_feature 2309..2313

QY	1381	GCAGCGTCTGAGAAGTCGGCAAAACACGTTTTCTGCTTGGTTGTATTTTGCTCTTTCGCTG	1440
DB	1381	GCAGCGTCGAGAAGTCGGCAAAACACGTTTTCTGCTTGGTTGTATTTTGCTCTTTCGCTG	1440
QY	1441	GTTCCCTCTTCACTTTAAGCCGTATATTGAAGAAAACACTGTATAACGAAATGACAAGAA	1500
DB	1441	GTTCCCTCTTCACTTTAAGCCGTATATTGAAGAAAACACTGTATAACGAAATGACAAGAA	1500
QY	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTATGGAATACATCGGTATTAACTTTGCCAAC	1560
DB	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTATGGAATACATCGGTATTAACTTTGCCAAC	1560
QY	1561	CATGAATTCATCTATAAACC CATAGCTCTGTATTTTGTGACGACAANAATTTAAAAATTG	1620
DB	1561	CATGAATTCATCTATAAACC CATAGCTCTGTATTTTGTGACGACAANAATTTAAAAATTG	1620
QY	1621	TFTCCAGTCATCCCTCTGCTGCTGTATTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
DB	1621	TFTCCAGTCATCCCTCTGCTGCTGTATTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
QY	1681	CATGAACGGAACAAGCATCCAGTGGAAAGAACACGATCAAAACACCAACACAGACCG	1740
DB	1681	CATGAACGGAACAAGCATCCAGTGGAAAGAACACGATCAAAACACCAACACAGACCG	1740
QY	1741	GAGCAGCCATAAGGACAGCATCACTGACCACCCCTTAGAGCACCTCTCGGTACTCCCAT	1800
DB	1741	GAGCAGCCATAAGGACAGCATCACTGACCACCCCTTAGAGCACCTCTCGGTACTCCCAT	1800
QY	1801	AATCCTCTCGGAGAAAAAATCACAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
DB	1801	AATCCTCTCGGAGAAAAAATCACAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860
QY	1861	CTTCTTCTTAATTCACTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
DB	1861	CTTCTTCTTAATTCACTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGGTAGA	1920
QY	1921	CTGGTTTATCCACCCACACACATCTAGGAATCGTACTTCTTAATGATCTAATTTACATA	1980
DB	1921	CTGGTTTATCCACCCACACACATCTAGGAATCGTACTTCTTAATGATCTAATTTACATA	1980
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DB	1981	TTCGCGTGTGTATTTCAGCACAATAAATGGTGGGAGCTGGGGAGAAATGAAGACTGTT	2040
QY	2041	AAATGAACACGAGGATATTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100
DB	2041	AAATGAACACGAGGATATTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100
QY	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCAACCATGAACCTTAG	2160
DB	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCAACCATGAACCTTAG	2160
QY	2161	AGATTACGACAGAATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCCAGCAAACACA	2220
DB	2161	AGATTACGACAGAATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCCAGCAAACACA	2220
QY	2221	ATATGGGCTCAGGTCACATTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGA	2280
DB	2221	ATATGGGCTCAGGTCACATTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAAGTGA	2280
QY	2281	TAATAGCCTAACATGATTTTGAACCTATTATTTACACATAGTTTGAAAAAAGACAAA	2340
DB	2281	TAATAGCCTAACATGATTTTGAACCTATTATTTACACATAGTTTGAAAAAAGACAAA	2340
QY	2341	AATAGTATTCAGGTGAGCAATTAGATTTAGTATTTTCCAGCTCACATTTATTTTTTAAA	2400
DB	2341	AATAGTATTCAGGTGAGCAATTAGATTTAGTATTTTCCAGCTCACATTTATTTTTTAAA	2400
QY	2401	ACACAAATTCATAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
DB	2401	ACACAAATTCATAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460

Qy	2461	TTTGGCAGTTTAAATAGATGTTTACTCAAGAAATTTTTTAAAGAACTGTATTTTAAATTTTTTAA	2520
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Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGCTTTTGATGTAAATTCAAAAGTAATGC	2580
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Qy	2641	AAAATCAATGCAAGTACGAAATGTTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
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Qy	2701	TCAGTGCACCTGTATATAGAAGTCTAAACACACACTTAAGAGAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATATAGAAGTCTAAACACACACTTAAGAGAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAATTTTCATTCAGSTATTGTAATAGTGACATATATATATATATACATAT	2820
Db	2761	ATGATTCGGAATTTTCATTCAGSTATTGTAATAGTGACATATATATATATATACATAT	2820
Qy	2821	CACCTCCATATCTTAAATTTTTTGTAAAATGTTTAACCTGGCAGTAAGTCTTTTGGTATCA	2880
Db	2821	CACCTCCATATCTTAAATTTTTTGTAAAATGTTTAACCTGGCAGTAAGTCTTTTGGTATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACT	2940
Db	2881	TTCCCTTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACT	2940
Qy	2941	GAAAAATAATTACCCACAAAATGCCACCACTAACTTAACGATTTCTTCACTCTTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAAATGCCACCACTAACTTAACGATTTCTTCACTCTTTGGGGTTT	3000
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Db	3001	TCAGTATGAACCTAACTCCCAACCCCAACATCTCCCTCCACATTTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAACTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCCCC	3180
Db	3121	AAAACTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCCCC	3180
Qy	3181	ATTTTCTTAGACTGTCTCTGGGAATATATTGTGTGTGATATATGTCATGTGTGAT	3240
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Qy	3241	GGTATGATGATTTAAATCTAAATTAATTTGTCCCGCAGTTGTGCCAAAGTGCAATA	3300
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Qy	3301	GTCTGAGCTAAAATCTAGGTGATTTTTCATCATGACAACCTGCCCTCAGTCCATTTTAAACC	3360
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Qy	3361	TGTAGCAACCTTCTGCATTCATAATCTTGTGAATCATGTTACCAATATAGGGCTTTGTTGGTGGT	3420
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Qy	3421	AGAGCGCGTGAAGCAGATGAGCTGGACTACCAATATAGGGCTTTGTTGGTGGT	3480
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Qy	3481	TGGTTTGATAAAGCAGTATTTTGGGGTCAATTTGTTCTGTCTCGTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTTGGGGTCAATTTGTTCTGTCTCGTGGAGCAAAAGTCATTA	3540
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 Db 3601 TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATGCTGATAATAAATAGTAAGATA 3660
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 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAGCCAGGCGCTGAGTTGGCAGTGGCCCAATAGTG 4080
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 Db 4081 TAAATAAAGTTTACAGAAACCTT 4105

RESULT 2
 AAA38341
 ID AAA38341 standard; DNA; 4105 BP.
 XX AC AAA38341;
 XX AC
 DT 21-AUG-2000 (first entry)
 XX DE Human endothelin receptor type A gene coding region.
 DE
 ...
 KW Endothelin receptor type A gene; coding region;
 KW polymorphism; polymorphic marker; cardiovascular disease;
 KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
 KW stroke; prognosis; drug screening; treatment outcome; human; ds.
 XX OS Homo sapiens.
 XX XX
 PN W0200022166-A2.
 XX XX
 PD 20-APR-2000.
 XX XX
 XX 13-OCT-1999; 99WO-IB01678.
 XX XX
 PR 14-OCT-1998; 98US-0104286.
 PR 14-OCT-1998; 98US-0104302.
 XX XX
 PA (EURO-) EURONA MEDICAL AB.
 XX XX
 PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
 XX XX
 DR WPI; 2000-318010/27.
 XX XX
 PT Assessing cardiovascular status in humans involves comparing test

PT polymorphic pattern comprising polymorphic positions within genes
 PT encoding specific proteins, with reference polymorphic pattern -
 XX Disclosure; Page 125-126; 126pp: English.
 XX
 CC The invention relates to a novel method of assessing the cardiovascular
 CC status in an individual and to newly identified polymorphisms in the
 CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
 CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
 CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
 CC receptors 1 and 2. The method comprises determining the sequence at one
 CC or more polymorphic positions within these genes, and comparing the
 CC pattern of polymorphisms from the individual with a reference polymorphic
 CC pattern obtained from a population of individuals exhibiting a
 CC predetermined cardiovascular disease status. The polymorphic markers are
 CC useful for determining the predisposition of an individual to
 CC cardiovascular disorders such as myocardial infarction, unstable angina,
 CC hypertension, atherosclerosis and stroke. They are also useful for
 CC predicting the likely cardiovascular status of a patient given a
 CC treatment regimen comprising administration of cardiovascular drugs
 CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
 CC blockers) or calcium channel blockers). One or more polymorphic markers
 CC provides a basis for predicting the outcome of a treatment regimen.
 CC Fragments of the genes comprising a polymorphic site may be used as
 CC primers and probes for detecting genetic polymorphisms or in molecular
 CC library arrays for high throughput screening. The genes, and the proteins
 CC they encode are useful in the screening of potential cardiovascular
 CC drugs. Determination of an individual's polymorphic pattern reduces or
 CC eliminates trial and error in selecting a treatment for a particular
 CC individual cardiovascular patient. It also provides the ability to
 CC eliminate patients from clinical trials who are predicted to be
 CC non-responsive, or at a risk for an adverse response, to a particular
 CC treatment regimen. Adverse results in an early trial can be evaluated to
 CC identify polymorphic patterns so that the adverse results can be
 CC correlated with a sub-population of the test population, permitting
 CC exclusion of such sub-populations from the treatment group. Beneficial
 CC drugs can be approved for use in the appropriate population, thereby
 CC decreasing the number of patients required for a clinical trial, which in
 CC turn decreases the duration and cost of such trials. The present
 CC sequence represents the human endothelin receptor type A gene
 CC coding region (GenBank S57498). The polymorphic sites identified are
 CC 969C/T, 1005A/G, 1146A/G and 2485T/C.
 XX
 SQ Sequence 4105 BP; 1138 A; 859 C; 843 G; 1263 T; 2 other;

Query Match Similarity 100.0%; Score 4103; DB 21; Length 4105;
 Best Local Similarity 100.0%; Fred. No. 0;
 Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 1 GAATTCGCGCGCCCTCTTGGTCCAGAGTGGAGTGAAGTCTGGAGCTTTGGGAGG 60
 Qy 61 AGACGGGAGGACACAGCTGGAGCGGTGTTCTCCGGAGTTTCTTTTCTCGAGCCCT 120
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 Qy 121 CGCGCGCGGTACAGTATCCCGCTGTGTCACGATTGTGGAGAGCGGTGGAGAGCTT 180
 Db 121 CGCGCGCGGTACAGTATCCCGCTGTGTCACGATTGTGGAGAGCGGTGGAGAGCTT 180
 Qy 181 CATCCATCCACCGGTCTGCGCGGGATTGGGTCCCGAGACACCTCCCGGGAGAA 240
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 Qy 301 CGGAGCCCGGACACCGGCCACCTCCCGCCACCCACCTCGCTTCTTCGGCTTCCTC 360
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Db 2521 ATGGTGTGTTTATTACAAGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGC 2580
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 Qy 2701 TCAGTGCACTGTATATAGAGTCTAAACACACACCTAAGAGAGAAAAGATCGAATTTTCAG 2760
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 Db 3001 TCAGTATGAACCTAATCTCCCAACCCCAACATCTCCCTCCCAATGTCCACATTTCAAG 3060
 Qy 3061 GGGCCACAGTACTTGTCTGGGCAATTTCCAGATGTTTACAGAGTGTGACACAGCAG 3120
 Db 3061 GGGCCACAGTACTTGTCTGGGCAATTTCCAGATGTTTACAGAGTGTGACACAGCAG 3120
 Qy 3121 AAAATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCC 3180
 Db 3121 AAAATCTTTTACTAGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCC 3180
 Qy 3181 ATTTTCTAGACTGTCTGTGGATATATTTGTGTGTGTATATATGATGTGTGTAT 3240
 Db 3181 ATTTTCTAGACTGTCTGTGGATATATTTGTGTGTGTATATATGATGTGTGTAT 3240
 Qy 3241 GGTATGTATGATTTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATA 3300
 Db 3241 GGTATGTATGATTTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATA 3300
 Qy 3301 GTCTGAGCTAAATCTAGGTGATTTGTCATCATGACAACCTGCCCTCAGTCCATTTTAACC 3360
 Db 3301 GTCTGAGCTAAATCTAGGTGATTTGTCATCATGACAACCTGCCCTCAGTCCATTTTAACC 3360
 Qy 3361 TGTAGCAACCTTCTGCATTCATAAATCTGTAAATCATGTTTACCATTTACAAATGGATATA 3420
 Db 3361 TGTAGCAACCTTCTGCATTCATAAATCTGTAAATCATGTTTACCATTTACAAATGGATATA 3420
 Qy 3421 AGAGCGACGTTGAAGCAGATGAGCTGTGGACTACATATAGGGTTTGTGTTGGT 3480
 Db 3421 AGAGCGACGTTGAAGCAGATGAGCTGTGGACTACATATAGGGTTTGTGTTGGT 3480
 Qy 3481 TGGTTTGTATAAGCAGATTTTGGGGTCAATTTGTTCTGTGCTGAGCAAAAGTCATTA 3540
 Db 3481 TGGTTTGTATAAGCAGATTTTGGGGTCAATTTGTTCTGTGCTGAGCAAAAGTCATTA 3540
 Qy 3541 CACTTTGAAGTATTAATTTGTTCTTATCCTCAATTTCAATTTGTTGATGAAATTTGCCAGGT 3600
 Db 3541 CACTTTGAAGTATTAATTTGTTCTTATCCTCAATTTCAATTTGTTGATGAAATTTGCCAGGT 3600
 Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTTGCTGATATAAATTTAGTGAAGATA 3660
 Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTTGCTGATATAAATTTAGTGAAGATA 3660

RESULT 3

AAL39858
 ID AAL39858 standard; DNA; 2595 BP.

XX AC AAL39858;

XX XX 05-SEP-2002 (first entry)

XX DE Human allergy-associated gene SEQ ID No 30.

XX KW Antiallergic; allergic disease; carboxypeptidase M; cathepsin C; CYP1B1;
 KW endoserine A receptor; osteoblast-specific factor 2; DD96; gene therapy;
 KW bronchial asthma; human; ds.

XX OS Homo sapiens.

XX PN WO200252006-A1.

XX XX 04-JUL-2002.

XX PF 21-DEC-2001; 2001WO-JP11287.

XX PR 26-DEC-2000; 2000JP-0396166.

XX XX (GENO-) GENOX RES INC.

XX PI Ohtani N, Matsui K, Yoshida N, Sugita Y, Izuhara K;

XX DR WPI; 2002-500763/53.

XX PT Examining allergic diseases by changes in expression levels of six
 PT allergy-associated genes inducible by stimulation e.g. of airway
 PT epithelia cells with interleukin-4 or 13, also applicable in screening
 compounds

XX PS Disclosure; Page 79-80; 106pp; Japanese.

XX CC The invention relates to a novel method for examining allergic diseases,
 comprising determining the expression level of a gene selected from

cc carboxypeptidase M, cathepsin C, endoserine A receptor, osteoblast-specific factor 2, DP96 and CYP1B1 in the biological sample from a patient, and comparing the expression level with that in the sample of a healthy individual. The polynucleotides of the invention can be used to treat disorders by gene therapy. The method is useful for examining allergic diseases particularly bronchial asthma and its diagnosis, which is also applicable in screening candidate compounds for remedies. This cc polynucleotide sequence represents a human allergy-associated gene of the invention.

xx
SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

	Query Match	60 2s; Score 2470; DB 24; Length 2595;
	Best Local Similarity 100.08; Pred. No. 0;	
	Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	1624 CCAGTCATGCCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGTAGACCTCGTCCGCCAT 1683	
-b	15 CCAGTCATGCCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGTAGACCTCGTCCGCCAT 74	
QY	1684 GAACGGAACAGCATCCAGTGGAGAACACACGATCAAAACACCAACACAGACCGGAG 1743	
Db	75 GAACGGAACAGCATCCAGTGGAGAACACGATCAAAACACCAACACAGACCGGAG 134	
QY	1744 CAGCCATAAGGACAGCATGAAGTACACCCCTTAGAAGCACTCCCGGTACTCCCATAT 1803	
Db	135 CAGCCATAAGGACAGCATGAAGTACACCCCTTAGAAGCACTCCCGGTACTCCCATAT 194	
QY	1804 CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCCT 1863	
Db	195 CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCCT 254	
QY	1864 CTTCTTAATTCACCTCCACACCCCAAGAAATGCTTTCCAAAACCGCAAGTAGACTG 1923	
Db	255 CTTCTTAATTCACCTCCACACCCCAAGAAATGCTTTCCAAAACCGCAAGTAGACTG 314	
QY	1924 GTTTATCCACCACCAACATCTACGAATCGTACTCTTTAAATGATCTAATTTACATATTC 1983	
Db	315 GTTTATCCACCACCAACATCTACGAATCGTACTCTTTAAATGATCTAATTTACATATTC 374	
QY	1984 TGCCTGTGTATTCAGCACTAAATAATGGTGGAGCTGGGGAGAAATGAAGACTGTTAA 2043	
Db	375 TGCCTGTGTATTCAGCACTAAATAATGGTGGAGCTGGGGAGAAATGAAGACTGTTAA 434	
QY	2044 TGAACACCAAGAGGATTTACTACTTTTCATGAAATAGAGCTTTCAAGTACATGGCTA 2103	
-b	435 TGAACACCAAGAGGATTTACTACTTTTCATGAAATAGAGCTTTCAAGTACATGGCTA 494	
QY	2104 GCTTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAGAGA 2163	
Db	495 GCTTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAGAGA 554	
QY	2164 TTAACGACAGATTTCTACTTTTAAAGTGATTTTGTGCTTCAGCCAAACACAATA 2223	
Db	555 TTAACGACAGATTTCTACTTTTAAAGTGATTTTGTGCTTCAGCCAAACACAATA 614	
QY	2224 TGGGCTCAGGTCACCTTTATTTGAAATGCTCATTTGGTGCCAGTATTTTAACTGCATA 2283	
Db	615 TGGGCTCAGGTCACCTTTATTTGAAATGCTCATTTGGTGCCAGTATTTTAACTGCATA 674	
QY	2284 TAGCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAATAAAAAAAGACAAAAAT 2343	
Db	675 TAGCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAATAAAAAAAGACAAAAAT 734	
QY	2344 AGTATTCAGGTGAGCAATAGATAGTATTTTCCACGTCACATAATTTTAAAAACA 2403	
Db	735 AGTATTCAGGTGAGCAATAGATAGTATTTTCCACGTCACATAATTTTAAAAACA 794	
QY	2404 CAAATTCATAGCTACACAAATACTACAGGCCCTTTAAAGCACAGTCTGATGACACATTT 2463	
Db	795 CAAATTCATAGCTACACAAATACTACAGGCCCTTTAAAGCACAGTCTGATGACACATTT 854	
QY	2464 GGCAGTTTAATAGATGTTACTCAAGAAATTTTAAAGAACTGTTATTTTAAATG 2523	

Db	855 GGCAGTTTAATAGATGTTACTCAAGAAATTTTAAAGAACTGTTATTTTAAATG 914
QY	2524 GTCTTTTATACAGGACCTTGAACATGTTTGTATGTTAAATCAAAAGTAATGCTTC 2583
Db	915 GTCTTTTATACAGGACCTTGAACATGTTTGTATGTTAAATCAAAAGTAATGCTTC 974
QY	2584 AATCAGATAGTCTCTTTTCAACAGTTCAATCACTGTTTTCATGTAATTTTGTATGAAA 2643
Db	975 AATCAGATAGTCTCTTTTCAACAGTTCAAT-CTGTTTTTTCATGTAATTTTGTATGAAA 1033
QY	2644 ATCAATGTCAGTACCAAAAATGTAATGTAATGTAATTAATTAATTAATTAATTAATTA 2703
Db	1034 ATCAATGTCAGTACCAAAAATGTAATGTAATGTAATTAATTAATTAATTAATTAATTA 1093
QY	2704 GTGCACGTGATATAGAGTCTAAACACACCTTAAGAGAAAAGATCAAAATTTTTCAGATG 2763
Db	1094 GTGCACGTGATATAGAGTCTAAACACACCTTAAGAGAAAAGATCAAAATTTTTCAGATG 1153
QY	2764 ATTCGGAATTTTTCATTCAGGTATTTGTAATAGTACATATATATATATATATATATAT 2823
Db	1154 ATTCGGAATTTTTCATTCAGGTATTTGTAATAGTACATATATATATATATATATATAT 1213
QY	2824 CTCCTATCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCATTC 2883
Db	1214 CTCCTATCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCATTC 1273
QY	2884 CTTTTTCCATATAGGAAACATATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTAA 2943
Db	1274 CTTTTTCCATATAGGAAACATATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTAA 1333
QY	2944 AAATAATTAACCCAAATGCCACCACTAACTTAACGATTTTCCACTCTTTGGGGTTTCA 3003
Db	1334 AAATAATTAACCCAAATGCCACCACTAACTTAACGATTTTCCACTCTTTGGGGTTTCA 1393
QY	3004 GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACTTGTCAACATTTTCAAGGGC 3063
Db	1394 GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACTTGTCAACATTTTCAAGGGC 1453
QY	3064 CCACAGTACTTTTGTGGGCAATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA 3123
Db	1454 CCACAGTACTTTTGTGGGCAATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA 1513
QY	3124 ATCTTTTACTAGTGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTACGCCATT 3183
Db	1514 ATCTTTTACTAGTGTGTGTGTATATATAAACAATTTGTAATTTCTTTTACGCCATT 1573
QY	3184 TTTCTAGACTGCTCTGTGGAATATATTTGTGTGTGTATATATATATATATATATATAT 3243
Db	1574 TTTCTAGACTGCTCTGTGGAATATATTTGTGTGTGTATATATATATATATATATATAT 1633
QY	3244 ATGATAGGATTTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC 3303
Db	1634 ATGATAGGATTTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC 1693
QY	3304 TGAGCTAAATCTAGGTGATTTTCATCATGACAACTCCCTCCCTAGTCCATTTTAACTGT 3363
Db	1694 TGAGCTAAATCTAGGTGATTTTCATCATGACAACTCCCTCCCTAGTCCATTTTAACTGT 1753
QY	3364 AGCAACCTTCTGCATTCATAAATCTTGAATCATGTACCATTACAAATGGGATATAAGA 3423
Db	1754 AGCAACCTTCTGCATTCATAAATCTTGAATCATGTACCATTACAAATGGGATATAAGA 1813
QY	3424 GGCAGCGTAAAGCAGATGAGCTGTGGACTAGCAATATAGGCTTTTGTGTTGGTGGTGG 3483
Db	1814 GGCAGCGTAAAGCAGATGAGCTGTGGACTAGCAATATAGGCTTTTGTGTTGGTGGTGG 1873
QY	3484 TTTGATAAAGCAGATTTTGGGTCATATGTTTCTGCTGGAGCAAAAGTCAATTAAC 3543
Db	1874 TTTGATAAAGCAGATTTTGGGTCATATGTTTCTGCTGGAGCAAAAGTCAATTAAC 1933
QY	3544 TTTGAGATTTATATATGTTCTTATCCCTCAATTCATGTTGGTGTGATGAAATGGCAGTTGT 3603

Db 1934 TTGAGGATATTATATTGTTCTTATCTCAATTCAGTGGTGATGAATAATGCCAGGTGT 1993
 Qy 3604 CTGATATTTCTTTTCAGACTCCGCCAGACAGATGCTGATAATAAATAGGTAAGATAATT 3663
 Db 1994 CTGATATTTCTTTTCAGACTCCGCCAGACAGATGCTGATAATAAATAGGTAAGATAATT 2053
 Qy 3664 TGTGGGCCATATTTTAGGACAGGTAAATTAACATCAGTTCCAGTTCCTGTAATTGCAA 3723
 Db 2054 TGTGGGCCATATTTTAGGACAGGTAAATTAACATCAGTTCCAGTTCCTGTAATTGCAA 2113
 Qy 3724 GGCTAAGAAGTACTGCCCTTTTGTGTGTAGCAGTCAAAATCTATTATTCCTACTGGCGCAT 3783
 Db 2114 GGCTAAGAAGTACTGCCCTTTTGTGTGTAGCAGTCAAAATCTATTATTCCTACTGGCGCAT 2173
 Qy 3784 CATATGCAAGTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTAT 3843
 Db 2174 CATATGCAAGTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTAT 2233
 Qy 3844 ATTGCTTTTTTTCAGAGTCTTTGTTTCTTTTCATATGAAAAAATGCAATTTATAAATT 3903
 Db 2234 ATTGCTTTTTTTCAGAGTCTTTGTTTCTTTTCATATGAAAAAATGCAATTTATAAATT 2293
 Qy 3904 CAGAAAGTCATAGATTTCTGAAGCGCTCAACGTGCATTTTATTTATGACGTGGTAAGTAA 3963
 Db 2294 CAGAAAGTCATAGATTTCTGAAGCGCTCAACGTGCATTTTATTTATGACGTGGTAAGTAA 2353
 Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCTAATTTTACCTTTTACTACATCTTTTCAACAAGT 4023
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCTAATTTTACCTTTTACTACATCTTTTCAACAAGT 2413
 Qy 4024 AACTTTGTAGAAATGAGCCAGCAAGCAAGGCCCTGAGTTGGCAGTGGCCCAATAAGTGTAA 4083
 Db 2414 AACTTTGTAGAAATGAGCCAGCAAGCAAGGCCCTGAGTTGGCAGTGGCCCAATAAGTGTAA 2473
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 4
 ABK94408
 ID ABK94408 standard; DNA: 2595 BP.
 XX
 AC ABK94408;
 XX
 XX 27-AUG-2002 (first entry)
 XX
 XX DNA encoding endothelin receptor A (EDNRA), exon 8.
 XX
 XX Endothelin; EDN; endothelin converting enzyme; ECE; EDNRA;
 XX endothelin receptor A; signaling system; cardiovascular disease;
 KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;
 KW fatty acid metabolism; diabetes; familial hypercholesterolemia;
 KW forensic marker; transgenic animal; solid support; SNP;
 KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH variation replace(1830,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 XX W0200224747-A2.
 XX
 XX 28-MAR-2002.
 PD
 XX 31-AUG-2001; 2001W0-EPI0087.
 XX
 XX 19-SEP-2000; 2000EP-0120123.
 XX
 XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 PA
 XX

PI Brinkmann U, Hoffmeyer S;
 XX WPI: 2002-435060/46.
 XX
 XX Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT treating the disease -
 XX
 PS Claim 1; Page -: 190pp; English.
 CC
 CC The invention describes a polynucleotide (I) of the endothelin
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 CC hypercholesterolemia. The gene or a polynucleotide fragment of the
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 CC creating a transgenic animal and in creation of a solid support
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 CC host cells of the invention. This sequence encodes the cardiovascular
 CC regulator Endothelin receptor A (EDNRA).
 CC Note: This sequence does not appear in the specification but has been
 CC obtained from GenBank using information given in the invention.
 XX
 SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match 60.2%; Score 2470; DB 24; Length 2595;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1624 CCAGTCATGCCCTCTGCTGCTGTGTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCAT 1683
 Db 15 CCAGTCATGCCCTCTGCTGCTGTGTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCAT 74
 Qy 1684 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACACACACACGGAG 1743
 Db 75 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACACACACACGGAG 134
 Qy 1744 CAGCCATAGGACACATGAATGACCAACCTTAGAAGCAGTCTCGGTACTCCCATAT 1803
 Db 135 CAGCCATAGGACACATGAATGACCAACCTTAGAAGCAGTCTCGGTACTCCCATAT 194
 Qy 1804 CTTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT 1863
 Db 195 CTTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT 254
 Qy 1864 CTTCTCTTAATTCACCTCCACACCCCAAGAAATGTTTCCAAAACCGAAGTAGACTG 1923
 Db 255 CTTCTCTTAATTCACCTCCACACCCCAAGAAATGTTTCCAAAACCGAAGTAGACTG 314
 Qy 1924 GTTTATCCCAACACATCTACGATCTGCTCTTTTAAATTCATCTAATTTACATATTC 1983
 Db 315 GTTTATCCCAACACATCTACGATCTGCTCTTTTAAATTCATCTAATTTACATATTC 374
 Qy 1984 TGCCTGTTGTATTTCAGCACTAAATAATGTTGGAGCTGGGGAGAAATGAAGACTGTAA 2043
 Db 375 TGCCTGTTGTATTTCAGCACTAAATAATGTTGGAGCTGGGGAGAAATGAAGACTGTAA 434
 Qy 2044 TGAACACAGAGATATTTTACTACTTTTTCATGAAATAGAGCTTTCAAGTACATGGCTA 2103

Db	435	TCGAACCAAGGATATTTACTACTTTTGCATGAAATAGAGCTTTTCAAGTACATACGCTA	494
Qy	2104	GCCTTTATGGCAGTCTCGTGAATGTTCAATGGGAACGTGTCACCACTGAACACTTTAGAGA	2163
Db	495	GCCTTTATGGCAGTCTCGTGAATGTTCAATGGGAACGTGTCACCACTGAACACTTTAGAGA	554
Qy	2164	TTAAGCACAGAATTTCTACTTTTTTTTAAAGTGATTTTTTGTCCCTCAGCCAAACACAATA	2223
Db	555	TTAAGCACAGAATTTCTACTTTTTTTTAAAGTGATTTTTTGTCCCTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACATTTTATTTGAAATGTCATTTTGGTGCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACATTTTATTTGAAATGTCATTTTGGTGCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAAGAAAAAAGACAAAAAT	2343
Db	675	TAGCCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAAGAAAAAAGACAAAAAT	734
Y	2344	AGTATTCAGGTGAGCAATTTAGTATTAGTATTTTCCAGCTCAGTACTATTTATTTTTTAAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTTAGTATTAGTATTTTCCAGCTCAGTACTATTTATTTTTTAAAAACA	794
Qy	2404	CAAAATTCCTAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAAATTCCTAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAGAAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAGAAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTGTTTATTACAAGGGACCTTTGAACATGTTTGTATGTTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTGTTTATTACAAGGGACCTTTGAACATGTTTGTATGTTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTTCACAAAGTTCAAATCTGTTTTTCATGTAAATTTTGTATGAAA	2643
Db	975	AATCAGATAGTTCTTTTTTTCACAAAGTTCAAAT - CTGTGTTTTTCATGTAATTTTGTATGAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATCTTAATGATGTGTCATTTAACTCTGCCTGAGACATTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATCTTAATGATGTGTCATTTAACTCTGCCTGAGACATTTCA	1093
Qy	2704	GTGCACCTGTATAGAAGTCTTAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACCTGTATAGAAGTCTTAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Y	2764	ATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCCTATCTCTAAATTTTGTGTTAAATCTGTTAACTGGCAGTAACTCTTTTTCATCATTC	2883
Db	1214	CTCCCTATCTCTAAATTTTGTGTTAAATCTGTTAACTGGCAGTAACTCTTTTTCATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTATTCATGTGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTATTCATGTGTCAGTGAA	1333
Qy	2944	AAATAAATTTACCCACAAAATGCCACAGTAACCTTAACAGATCTTCACATCTTTGGGGTTTTCA	3003
Db	1334	AAATAAATTTACCCACAAAATGCCACAGTAACCTTAACAGATCTTCACATCTTTGGGGTTTTCA	1393
Qy	3004	GTATCAACCTTAACCTCCACACCAACATCTCCCTCCACATCTGCACCACTTTCAAGGGC	3063
Db	1394	GTATGAACCTTAACCTCCACACCAACATCTCCCTCCACATCTGCACCACTTTCAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCCCATTT	3183
Db	1514	ATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCCCATTT	1573

RESULT 5
ABK35492
ID ABK35492 standard; DNA; 2595 BP.
XX
AC ABK35492;
XX
DT 08-MAY-2002 (first entry)

XX	Human endometrial cancer related gene, EDNRA.
DE	Human; ds; gene; endometrial cancer; differential expression;
XX	DNA microarray; protein microarray.
KW	Homo sapiens.
OS	W0200209573-A2.
XX	07-FEB-2002.
PN	31-JUL-2001; 2001WO-US24104.
XX	31-JUL-2000; 2000US-221735P.
PR	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX	Mutter GL;
PI	WPI; 2002-179967/23.
XX	P-PSDB; AAU84272.
XX	Diagnosing endometrial cancer comprises determining expression of
PT	nucleic acid molecules or expression products that are differentially
PT	expressed in normal and malignant endometrium -
XX	Claim 1; Page 60-62; 233pp; English.
PS	The invention relates to diagnosing endometrial cancer in a subject
XX	suspected of having endometrial cancer comprising determining the
CC	expression of a set of nucleic acid molecules or expression products in
CC	an endometrial sample suspected of being cancerous, where the set of
CC	nucleic acid molecules comprises at least 2 nucleic acid molecules
CC	selected from 50 fully defined sequences as given in the specification.
CC	The nucleic acids are used as an array of at least 2 of the 50
CC	nucleic acids bound to a solid substrate. Also included is a solid-phase
CC	protein microarray comprising at least 2 antibodies or its antigen
CC	binding fragments, that specifically bind at least 2 different
CC	polypeptides from the 50 fully defined sequences as given in the
CC	specification, fixed to a solid substrate. The methods and arrays are
CC	useful for the diagnosis of endometrial cancer, selecting and monitoring
CC	treatment regimes and identification of lead compounds useful for the
CC	treatment of endometrial cancer. The present sequence is one of 50
CC	genes differentially expressed between cancerous and non-cancerous
CC	samples.
XX	Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;
XX	Query Match 60.2%; Score 2470; DB 24; Length 2595;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1624 CCAGTCATGCTCTGCTGCTCTTTACCAGTCAAAAAGTCTGATGACCTCGGTCCCAT 1683
DB	15 CCAAGTCATGCTCTGCTGCTCTTTACCAGTCAAAAAGTCTGATGACCTCGGTCCCAT 74
QY	1684 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACCAACACAGACCCGAG 1743
DB	75 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACCAACACAGACCCGAG 134
QY	1744 CAGCCATAAGACAGCATGAACGTGACCAACCCCTTAGAAGCACTCCTCGGTACTCCGATAAT 1803
DB	135 CAGCCATAAGACAGCATGAACGTGACCAACCCCTTAGAAGCACTCCTCGGTACTCCGATAAT 194
QY	1804 CCTCTCGGAGAAAAAATACAGAGCAACTGTGACTCGGGAAATCTCTTCTGATCCTT 1863
DB	195 CCTCTCGGAGAAAAAATACAGAGCAACTGTGACTCGGGAAATCTCTTCTGATCCTT 254
QY	1864 CTTCCTTAATTACTCCACACCAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 1923
DB	255 CTTCCTTAATTACTCCACACCAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 314

Db	1394	GTATGAACCTAACTCCCAACCCCAACATCTCCCTCCACATTCGTCCCAATTCGTCAACATTTCAAGGGC	1453
Qy	3064	CCACAGTGAATTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGAATTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCCCAT	3183
Db	1514	ATCTTTTACTAGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCCCAT	1573
Qy	3184	TTTCTAGACTGTCTGTGGGAATATATTTGTGTGTGATATATGATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTGTGGGAATATATTTGTGTGTGATATATGATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTAATCTAATCTAATAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTAATCTAATCTAATAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAATCTAGGTGATTTCTCATCATGACAACTGCCTCAGTCCATTTTAACTGT	3363
Db	1694	TGAGCTAAATCTAGGTGATTTCTCATCATGACAACTGCCTCAGTCCATTTTAACTGT	1753
Qy	3364	AGCAACCTTCTGCATTCATAAATCTTGTAATCATGTATACCATTTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCATAAATCTTGTAATCATGTATACCATTTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTGGTGGTGG	3483
Db	1814	GGCAGCTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTGGTGGTGG	1873
Qy	3484	TTTGATAAGCAGTATTTGGGGTGCATATTTGTTCTCTGTCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAGCAGTATTTGGGGTGCATATTTGTTCTCTGTCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATTTGTTCTTATCCTCAATTCATGTGGTGATGAAATTTGCCAGTTGT	3603
Db	1934	TTTGAAGTATTATTTGTTCTTATCCTCAATTCATGTGGTGATGAAATTTGCCAGTTGT	1993
Qy	3604	CTGATATTTCTTACAGACTCGCCAGACAGATTCGTGATAATAAATTAGTAAAGTAAT	3663
Db	1994	CTGATATTTCTTACAGACTCGCCAGACAGATTCGTGATAATAAATTAGTAAAGTAAT	2053
Qy	3664	TGTTGGGCCATATTTTAGCAGAGTAAATTAACATCAGGTTCCAGTTGCTGAAATTTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGCAGAGTAAATTAACATCAGGTTCCAGTTGCTGAAATTTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCCCTTTTGTGTGTAGCAGTCAAATCTATTATTCACCTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCCCTTTTGTGTGTAGCAGTCAAATCTATTATTCACCTGGCGCAT	2173
Qy	3784	CATATGAGTGCATATATGCCCTATAATAAGCCATAGGTTACACACCATTTTGTGTAGACA	3843
Db	2174	CATATGAGTGCATATATGCCCTATAATAAGCCATAGGTTACACACCATTTTGTGTAGACA	2233
Qy	3844	ATTGCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCAATTTTATAAAT	3903
Db	2234	ATTGCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCAATTTTATAAAT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCAATTTTATTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCAATTTTATTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTACGAGGAATATTTCCTAATTTCTACCTTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTACGAGGAATATTTCCTAATTTCTACCTTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACCTTTAGAAAATGAGCCAGAACCAAGGCCCTGAGTTGGCAGTGGCCCAAGTGTAA	4083
Db	2414	AACCTTTAGAAAATGAGCCAGAACCAAGGCCCTGAGTTGGCAGTGGCCCAAGTGTAA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT 4105	

Db 2474 AATRAAGTTTACAGAAACCTT 2495

RESULT 6
AAFD0903
ID AAF20903 standard; DNA; 1868 BP.
XX AC
XX AC AAF20903;
XX DT 14-MAR-2001 (first entry)
XX
XX DE Human low adenosine antisense oligonucleotide #2470.
XX
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200062736-A2.
XX
XX PD 26-OCT-2000.
XX
XX PF 24-MAR-2000; 2000WO-US08020.
XX
XX PR 06-APR-1999; 99US-0127958.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX
XX PI Nyce JW;
XX
XX DR WPI; 2000-679539/66.
XX
XX PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX PS Disclosure; Page 676; 1592pp; English.
XX
XX CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
CC the antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with the
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC

CC and/or cancer, AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX WO2000062736-A2.
 PN 26-OCT-2000.
 XX
 PD 24-MAR-2000; 2000WO-US08020.
 PF 06-APR-1999; 99US-0127958.
 XX
 X (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PA
 XX
 PI Nyce JW;
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 244; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;
 Best Local Similarity 99.7%; Pred No. 0;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 421 AAAAAGTGAAGGTGTAAGACGACCAAGTGCATAAGAGATATTTCCCAAATTTGCCCT 480
 Db 10 AAAAAGTGAAGGTGTAAGACGACCAAGTGCATAAGAGATATTTCCCAAATTTGCCCT 69

QY 481 CAAGATGGAAACCCCTTTGGCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGAAT 540
 Db 70 CAAGATGGAAACCCCTTTGGCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGAAT 129
 QY 541 CAGTGTATTCCTTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCCACAC 600
 Db 130 CAGTGTATTCCTTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCCACAC 189
 QY 601 TTTTCTGTCACAGACTCAGCTTCCCTGGTACCACCTCATCAACCCACTAATTTGGTCCCT 660
 Db 190 TTTTCTGTCACAGACTCAGCTTCCCTGGTACCACCTCATCAACCCACTAATTTGGTCCCT 249
 QY 661 ACCAGCAATGGCTCAATGCACAACTATTGCCACACAGACTAAAATTTACTTCAGCTTT 720
 Db 250 ACCAGCAATGGCTCAATGCACAACTATTGCCACACAGACTAAAATTTACTTCAGCTTT 309
 QY 721 CAAATACATTAAACACTGTGTATCTTGTACTATTTTTCATCGTGGGAATGTTGGGAATGC 780
 Db 310 CAAATACATTAAACACTGTGTATCTTGTACTATTTTTCATCGTGGGAATGTTGGGAATGC 369
 QY 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGCCCCACGCGCTGAT 840
 Db 370 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGCCCCACGCGCTGAT 429
 QY 841 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATTCCTCCTATCAATGTATT 900
 Db 430 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATTCCTCCTATCAATGTATT 489
 QY 901 TAAGCTGCTGGCTGGGCGCTGGGCTTTTGTATCAACAATGACTTTTGGCGTATTTCTTTCGAA 960
 Db 490 TAAGCTGCTGGCTGGGCGCTGGGCTTTTGTATCAACAATGACTTTTGGCGTATTTCTTTCGAA 549
 QY 961 GCTGTTCCCTTTTGGAGAAAGTCTCCTGGTGGGATCAGCTCCTCAACCTCTCGGCTCT 1020
 Db 550 GCTGTTCCCTTTTGGAGAAAGTCTCCTGGTGGGATCAGCTCCTCAACCTCTCGGCTCT 609
 QY 1021 TACTGTTGACAGGTACAGACAGCTGCTCCTCGAGTCTGTTTTCAGGGAATTTGGGATTC 1080
 Db 610 TACTGTTGACAGGTACAGACAGCTGCTCCTCGAGTCTGTTTTCAGGGAATTTGGGATTC 669
 QY 1081 TTTGGTAACTGCCATGAAATTTGTCATCTGGATCCTGTCCTTTATPCTGGCCATTC 1140
 Db 670 TTTGGTAACTGCCATGAAATTTGTCATCTGGATCCTGTCCTTTATPCTGGCCATTC 729
 QY 1141 TGAAGCGATGGCTTCGTATGTCATGTCACCTTTGAATATAGGGGTGAACAGCATAAACCTG 1200
 Db 730 TGAAGCGATGGCTTCGTATGTCATGTCACCTTTGAATATAGGGGTGAACAGCATAAACCTG 789
 QY 1201 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAGGACTGGTGGCT 1260
 Db 790 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAGGACTGGTGGCT 849
 QY 1261 CTTCCGGGTTCTATTTCGTATGTCCTTTGGTGGCACTGCGATCTTACACCCCTCATGAC 1320
 Db 850 CTTCCGGGTTCTATTTCGTATGTCCTTTGGTGGCACTGCGATCTTACACCCCTCATGAC 909
 QY 1321 TTGTGAGATGTTGAACAGAGAGGAATGCGACCTTGAGAAATTCCTCCTCAGTGAACATCTTAA 1380
 Db 910 TTGTGAGATGTTGAACAGAGAGGAATGCGACCTTGAGAAATTCCTCCTCAGTGAACATCTTAA 969
 QY 1381 GCAGCGTCGAGAGAGTGGCAAAACAGTTTCTGCTGTTGTAATTTTGGCTCTTTGGCTG 1440
 Db 970 GCAGCGTCGAGAGAGTGGCAAAACAGTTTCTGCTGTTGTAATTTTGGCTCTTTGGCTG 1029
 QY 1441 GTTCCCTCTTCACTTAAGCGGTATATTGAAGAAACCTGTGTATTAACGAAATGGAAGAA 1500
 Db 1030 GTTCCCTCTTCACTTAAGCGGTATATTGAAGAAACCTGTGTATTAACGAGATGGAAGAA 1089
 QY 1501 CCGATGTGAATTAATTAATTTCTTACTGCTCATCGGATTAATTAATTTGGAAC 1560
 Db 1090 CCGATGTGAATTAATTAATTTCTTACTGCTCATCGGATTAATTAATTTGGAAC 1149
 QY 1561 CATGAATTCATGTATAAACCCCATGCTCTGTATTGTTGTGAGCAAGAAATTTAAATTTG 1620

QY	781	AAC	CTGCTGCTCAGGATCATTTACAGAACAAATCTATCAGCAATGGCCCCAACGGCTGAT	840
DB	370	AACT	CTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCCAACGGCTGAT	429
QY	841	AGCC	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCTATCAATGTAAT	900
DB	430	AGCC	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCTATCAATGTAAT	489
QY	901	TAA	GCTGCTGGCTGGCGGCTGGCCTTTTGATACAAATGACTTTGGCGGTATTTCTTTGCCAA	960
DB	490	TAA	GCTGCTGGCTGGCGGCTGGCCTTTTGATACAAATGACTTTGGCGGTATTTCTTTGCCAA	549
QY	961	GCT	GTGTTCCCTTTTTCGCAAGTCCTCGGTGGGGATCACCGTCTCAACCTCTGCGCTCT	1020
DB	550	GCT	GTGTTCCCTTTTTCGCAAGTCCTCGGTGGGGATCACCGTCTCAACCTCTGCGCTCT	609
QY	1021	TAG	TGTTGACAGGTACAGAGCAGTTGCCCTCTCGAGTCGTGTTCACGGGAATTCGGGATTC	1080
DB	610	TAG	TGTTGACAGGTACAGAGCAGTTGCCCTCTCGAGTCGTGTTCACGGGAATTCGGGATTC	669
QY	1081	TTT	TGTTAACTGCCATTGAAATTTGTCCTCATCTGGATCTCTCTTTATCTGCGCCATTC	1140
DB	670	TTT	TGTTAACTGCCATTGAAATTTGTCCTCATCTGGATCTCTCTTTATCTGCGCCATTC	729
QY	1141	TGA	AGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAAACCTG	1200
DB	730	TGA	AGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAAACCTG	789
QY	1201	TAT	GCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGACTGTGGGT	1260
DB	790	TAT	GCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGACTGTGGGT	849
QY	1261	CTT	CGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTCTACACCTCATGAC	1320
DB	850	CTT	CGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTCTACACCTCATGAC	909
QY	1321	TTG	TGAGATGTTGAACAGAAAGTGGCAGCTTGAGATTGCCCTCAGTGAACATCTTAA	1380
DB	910	TTG	TGAGATGTTGAACAGAAAGTGGCAGCTTGAGATTGCCCTCAGTGAACATCTTAA	969
QY	1381	CGA	CGTCGAGAGTGGCAAAACAGTTTCTGCTGGTTGTAATTTTGTCTTTGCTG	1440
DB	970	CGA	CGTCGAGAGTGGCAAAACAGTTTCTGCTGGTTGTAATTTTGTCTTTGCTG	1029
QY	1441	GTC	CCCTCTTCACTTAAAGCGTATATTGAAGAAAACCTGTGTATACGAAATGGACAAGAA	1500
DB	1030	GTC	CCCTCTTCACTTAAAGCGTATATTGAAGAAAACCTGTGTATACGAAATGGACAAGAA	1089
QY	1501	CCG	ATGTGAATTTACTTTTCTACTGCTCATGATATACATCGGTATTAACCTTGGCAAC	1560
DB	1090	CCG	ATGTGAATTTACTTTTCTACTGCTCATGATATACATCGGTATTAACCTTGGCAAC	1149
QY	1561	CAT	GAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGCAAGAAATTTAAAAATTG	1620
DB	1150	CAT	GAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGCAAGAAATTTAAAAATTG	1209
QY	1621	TTT	CAGTCATGCCCTCTGCTGCTGTATACAGTCCAAAAGTCTGTATGACCTCGGTCCC	1680
DB	1210	TTT	CAGTCATGCCCTCTGCTGCTGTATACAGTCCAAAAGTCTGTATGACCTCGGTCCC	1269
QY	1681	CAT	GAACGGAACAGCATCCAGTGAAGAACACAGCATCAAAACACCAACAGACAGCG	1740
DB	1270	CAT	GAACGGAACAGCATCCAGTGAAGAACACAGCATCAAAACACCAACAGACAGCG	1329
QY	1741	GAG	CAGCATTAAGGACAGCATGACCTGACCCCTTAGAGCACTCTCGGTACTCCCAT	1800
DB	1330	GAG	CAGCATTAAGGACAGCATGACCTGACCCCTTAGAGCACTCTCGGTACTCCCAT	1389
QY	1801	AAT	CCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCGGGGAATCTCTTCTCTGATC	1860
DB	1390	AAT	CCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCGGGGAATCTCTTCTCTGATC	1449
QY	1861	CTT	CTCTCTTAATCTACCTCCACACCCCAAGAGAAATGCTTTCCAAAACCCGAA-GGTAG	1919

Db	1450	CTTCTCTCTTAATTACATCCACACCCAAAGAAATGCTTCCAAACCGCAAGSGTAG	1509
Qy	1920	ACTGGTTATCCACCACCAACATCTACGAATCGTACTTCTTTAAATTGATCTAATTACAT	1979
Db	1510	ACTGGTTATCCACCACCAACATCTACGAATCGTACTTCTTTAAATTGATCTAATTACAT	1569
Qy	1980	ATTCTGCGTGTGTATTTCAGCACTTAAAAAATGGTGGGAGCTGGGGAGGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTGTATTTCAGCACTTAAAAAATGGTGGGAGCTGGGGAGGAATGAAGACTGT	1629
Qy	2040	TAAATGAACACCAAGAGATATTACTACTTTTGCATGAAAAATAGAGCTTTCAAAGTACATG	2099
Db	1630	TAAATGAACACCAAGAGATATTACTACTTTTGCATGAAAAATAGAGCTTTCAAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACCTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACCTTTA	1749
Qy	2160	GAGATTACGGACAAGATTCTTACTTTTTTTTAAAGTGA-TTTTTTGTCCTTCAGCCAAACA	2218
Db	1750	GAGATTACGGACAAGATTCTTACTTTTTTTTAAAGTGA-TTTTTTGTCCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACCTTTTATTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACTTTTATTGAAATGTCATTTGGTGCCAGTAT	1859

RESULT. 9

RESUL: 3
AAA34793

AAA34793
ID AAA34793 standard: DNA: 1868 bp.

XX
XX

AC AAA34793;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2482.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

lung disease; ischaemic condition; pulmonary vasoconstriction; asthma

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hyp

KW cancer; Leukaemia

50	XX
50	XX

US
Homo sapiens.
XX

YY
PN W0200009525-A

XX
PN
W0Z0000ZOM A-27C60000ZOM

24-FEB-2000

XX
FD 24-FEB-2000.

03-AUG-1999.

03-AUG-1955, 95MO-QMST//12.
FF XX

PR 03-AUG-1998: 98TIS-0095212

XX
XX
00 400 1000, 0000 000000.

PA (UYEC-) UNIV EAST CAROLINA.

[illegible]

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

inflammation. The ON can have antiinflammatory, antiallergic, antisthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 195, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match	44.3%;	Score 1819.6;	DB 21;	Length 1868;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1844;	Conservative	0;	Mismatches	4;
				Index's 2.

Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 421 AAAAAGTGAAGGTGTAAAGCAGCACAAAGTGCATAAGAGATATTTCTCCTCAAAATTTGCCT 480
 |||||
 Db 10 AAAAAGTGAAGGTGTAAAGCAGCACAAAGTGCATAAGAGATATTTCTCCTCAAAATTTGCCT 69

Qy	481	CAAGATGGAAACCCCTTTG CCTCAGGGCATCCTTTTGGCTGGCAC TGCGTTGGATGTGAAT	540
Db	70	CAAGATGGAAACCCCTTTG CCTCAGGGCATCCTTTTGGCTGGCAC TGCGTTGGATGTGAAT	129

Qy	541	CAGTGATAATCCTGGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCACCAC	600
	130	CAGTGATAATCCTGGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCACCAC	189
Db			

Qy	601	TTTTCGTGGCAGAGCTCAGCTTCTCGGTTACCACTCATCAACCACCTAATTTGGTGCT	660
Db	190	TTTTCGTGGCAGAGCTCAGCTTCTCGGTTACCACTCATCAACCACCTAATTTGGTGCT	249

Qy	661	ACCCAGCAATGGCTCAAATGCACAACACTATTGCCCACAGCAGACTAAAATTACTTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAAATGCACAACACTATTGCCCACAGCAGACTAAAATTACTTTCAGCTTT	309

721 CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGCTGGGGGAATGC 780
|||||
310 CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGCTGGGGGAATGC 360

QY 781 AACTCTGTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGGTGAT 840
|||||
Db 370 AACTCTGTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGGTGAT 420

Qy 841 AGCCAGCTTGGCCCTTGGACACCTTATCTATGTGGTCATTTGATCTCCCTATCAATGTAATT 900
|||||
Db 430 AGCCAGCTTGGCCCTTGGACACCTTATCTATGTGGTCATTTGATCTCCCTATCAATGTAATT 480

Oy 901 TAAGCTGCTGGCGGTGGCCATTTCATCACAACACTTGGCGTAATTCTTTGCCA 960
|||
dh 480 TAAAGCTGCATCCCCCATCCCCCCCCTTTTTTGCTCACTCACGCTGAATGCTGCTGCT

QY 961 GGTGTTCCCTTTTTCAGAACTCCTCGGTGGGATCACCGTCTCTCAACCTCTGGGCTCT 102

QY 1021 TAGTGTTCACAGGTACAGACAGTTGCCTCCTGGAGTCGTGTTACAGGGAAATTGGCATTC 108

[illegible]

QY	1081	TTTGGTAACTGC	CAATGAAAT	TGCTCCATCTGG	ATCTGCTCTGCTTTATCTGG	CAATTC	1140
DB	670	TTTGGTAAC	TGCCATGAAAT	TGCTCCATCTGG	ATCTGCTCTGCTTTATCTGG	CAATTC	729
QY	1141	TGAAGCGATTGG	CTTCGTATGTTG	ATATAGGG	GTGAACAGCATAA	AACCTG	1200
DB	730	TGAAGCGATTGG	CTTCGTATGTTG	ATATAGGG	GTGAACAGCATAA	AACCTG	789
QY	1201	TATGCTCAATG	CCACATCAAA	ATTCATGG	AGTTCACCAAGATG	TAAAGAC	1260
DB	790	TATGCTCAATG	CCACATCAAA	ATTCATGG	AGTTCACCAAGATG	TAAAGAC	849
QY	1261	CTTCGGGTTCT	ATTTCTGTATGCC	TTGGTGC	ACTGCGATCTT	CATACACCTCAT	1320
DB	850	CTTCGGGTTCT	ATTTCTGTATGCC	TTGGTGC	ACTGCGATCTT	CATACACCTCAT	909
QY	1321	TTGTGAGATG	TTGAACAG	AAGGAATGC	AGCTTTGAGA	ATTCGCTCAGTGAACATCTTAA	1380
DB	910	TTGTGAGATG	TTGAACAG	AAGGAATGC	AGCTTTGAGA	ATTCGCTCAGTGAACATCTTAA	969
QY	1381	GCAGCCTCG	AGAGTGG	CAAAAACAG	TTTTCTGCTGG	TGTAAATTTTTCCTCTTGC	1440
DB	970	GCAGCCTCG	AGAGTGG	CAAAAACAG	TTTTCTGCTGG	TGTAAATTTTTCCTCTTGC	1029
QY	1441	GTTCCTCTT	CACTTAAG	CGGTATATGA	AGAAAAC	TGCTATTAACGAAATG	1500
DB	1030	GTTCCTCTT	CACTTAAG	CGGTATATGA	AGAAAAC	TGCTATTAACGAAATG	1089
QY	1501	CGGATCGA	ATTACTT	AGTTTCTT	ACTGCTCAT	GGAATACATCGG	1560
DB	1090	CGGATCGA	ATTACTT	AGTTTCTT	ACTGCTCAT	GGAATACATCGG	1149
QY	1561	CATGAATCAT	GATATAAAC	CCCAATG	CTGTATTTGTG	AGCAAGAAATTTAA	1620
DB	1150	CATGAATCAT	GATATAAAC	CCCAATG	CTGTATTTGTG	AGCAAGAAATTTAA	1209
QY	1621	TTTCCAGT	CATGCTCTG	CTGCTG	TTACCA	AGTCCAAAAGTCTGAT	1680
DB	1210	TTTCCAGT	CATGCTCTG	CTGCTG	TTACCA	AGTCCAAAAGTCTGAT	1269
QY	1681	CATGAACG	GAACAAG	CATCCAG	TGGGAAG	CAACACGATCAAA	1740
DB	1270	CATGAACG	GAACAAG	CATCCAG	TGGGAAG	CAACACGATCAAA	1329
QY	1741	GAGCAGC	CAATAGG	CACAGATG	NACTGAC	CCCTTAGAG	1800
DB	1330	GAGCAGC	CAATAGG	CACAGATG	NACTGAC	CCCTTAGAG	1389
QY	1801	AATCTCT	CCGAGAAAA	AATCAC	AGGCAACTG	TGACTCCGG	1860
DB	1390	AATCTCT	CCGAGAAAA	AATCAC	AGGCAACTG	TGACTCCGG	1449
QY	1861	CTTCTTCT	TAATTACT	CCACAC	CCCAAG	AGAAATGCTTTCC	1919
DB	1450	CTTCTTCT	TAATTACT	CCACAC	CCCAAG	AGAAATGCTTTCC	1509
QY	1920	ACTGGTTAT	TCCACC	CAACATCT	ACGAATCGT	ACTCTTTAA	1979
DB	1510	ACTGGTTAT	TCCACC	CAACATCT	ACGAATCGT	ACTCTTTAA	1569
QY	1980	ATTCTG	CGTTGTAT	CTAC	ACTAAAA	ATGGGAGCTGGG	2039
DB	1570	ATTCTG	CGTTGTAT	CTAC	ACTAAAA	ATGGGAGCTGGG	1629
QY	2040	TAATTAAC	ACAGAG	AGGATATTT	ACTACTTT	TTCATGAAATAG	2099
DB	1630	TAATTAAC	ACAGAG	AGGATATTT	ACTACTTT	TTCATGAAATAG	1689
QY	2100	GCTAGCTTT	TATGG	CAGTTCTG	GTAACTG	CAATGGGA	2159
DB	1690	GCTAGCTTT	TATGG	CAGTTCTG	GTAACTG	CAATGGGA	1749
QY	2160	GAGATTA	ACGACA	AGATTTT	CTACTTTTT	TAAAGTGA	2218

Db 1750 GAGATTAAACACAGATTTTCTACTTTTAAAGTGATTTTCTTCTCAGCCAAACA 1809
 QY 2219 CAATATGGGCTCAGTCACTTTTATTTGAATGTCATTTGGTGGCAGTAT 2268
 Db 1810 CAATATGGGCTCAGTCACTTTTATTTGAATGTCATTTGGTGGCAGTAT 1859

RESULT 10
 AAF20904
 ID AAF20904 standard; DNA; 2008 BP.
 XX AAF20904;
 XX AAF20904;
 DT 14-MAR-2001 (first entry)
 XX Human low adenosine antisense oligonucleotide #2471.
 W Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 OS Wo2000062736-A2.
 PN 26-OCT-2000.
 XX 24-MAR-2000; 2000WO-US08020.
 PF 06-APR-1999; 99US-0127958.
 PR (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI Nyce JW;
 XX WPI; 2000-679539/66.
 XX Low adenosine (A) content antisense oligonucleotides which do not
 trigger adenosine receptors during metabolism, useful e.g. for treating
 cancers and respiratory obstructions -
 XX Disclosure; Page 676-677; 1592pp; English.
 XX The present invention describes low adenosine (A) content antisense
 oligonucleotides and compositions (I) comprising them. In the antisense
 oligonucleotides the A is replaced by a 'Universal' or alternative base.
 (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 The antisense oligonucleotides and (I) can be used to down-regulate the
 expression and or activity of target polypeptides associated with
 lung/respiratory disorders and malignancies, such as stimulating and
 activating peptide factors and transmitters, transcription factors,
 immunoglobulins and antibodies, antibody receptors, cytokines and
 chemokines, endogenously produced specific and non-specific enzymes,
 binding proteins, adhesion molecules and their receptors, cytokine and
 chemokine receptors, adenosine receptors, bradykinin receptors, central
 nervous system (CNS) and peripheral nervous and non-nervous system
 receptors, CNS and peripheral nervous and non-nervous system peptide
 transmitters, defensins, growth factors, vasoactive peptides and
 receptors, binding proteins and malignancy associated proteins. The
 antisense oligonucleotides may be used in this way to treat disorders
 including respiratory obstruction (especially pulmonary obstruction
 and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 2008 BP; 563 A; 463 C; 416 G; 566 T; 0 other;
 Query Match 44.3%; Score 1819.6; DB 21; Length 2008;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 QY 421 AAAAAGTGAAGGTGTAAAGAGCAGCAACAGTGCATTAAGAGATATTTCTCAAAATTTGCCT 480
 Db 150 AAAAAGTGAAGGTGTAAAGAGCAGCAACAGTGCATTAAGAGATATTTCTCAAAATTTGCCT 209
 QY 481 CAAGATGGAACCCCTTTGCCCTCAGGGGATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 540
 Db 210 CAAGATGGAACCCCTTTGCCCTCAGGGGATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 269
 QY 541 CAGTGATAATCTCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC 600
 Db 270 CAGTGATAATCTCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC 329
 QY 601 TTTTCGTGGCAGAGCTCAGCTTCTCTGTATACCACTCATCAACCCAGCTAAATTTGGTCT 660
 Db 330 TTTTCGTGGCAGAGCTCAGCTTCTCTGTATACCACTCATCAACCCAGCTAAATTTGGTCT 389
 QY 661 ACCCAGCAATGGCTCAATGACACACTATTTGCCACAGCAGACTAAATTTACCTTACCTT 720
 Db 390 ACCCAGCAATGGCTCAATGACACACTATTTGCCACAGCAGACTAAATTTACCTTACCTT 449
 QY 721 CAATACATTAACACTGTGATATCTTGTACTATTTTCTATCTGGGAAATGGTGGGAAATGC 780
 Db 450 CAATACATTAACACTGTGATATCTTGTACTATTTTCTATCTGGGAAATGGTGGGAAATGC 509
 QY 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATAGGAATGCCCAACCCGCTGAT 840
 Db 510 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATAGGAATGCCCAACCCGCTGAT 569
 QY 841 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATTCCTTATCAATGATTT 900
 Db 570 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATTCCTTATCAATGATTT 629
 QY 901 TAAGCTCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACCTTTGGCGTATTTCTTTGCA 960
 Db 630 TAAGCTCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACCTTTGGCGTATTTCTTTGCA 689
 QY 961 GCTGTTCCCTTTTTCAGAGAGTCTCTGGTGGGATCACCCTCCTCAACCTCTCGGCTCT 1020
 Db 690 GCTGTTCCCTTTTTCAGAGAGTCTCTGGTGGGATCACCCTCCTCAACCTCTCGGCTCT 749
 QY 1021 TAGTGTTCAGAGTTCAGAGACAGTTCCTCTCTGGAGTCTGTTTTCAGGAAATTTGGGATTC 1080
 Db 750 TAGTGTTCAGAGTTCAGAGACAGTTCCTCTCTGGAGTCTGTTTTCAGGAAATTTGGGATTC 809
 QY 1081 TTTGGTGAACCTGCCATTCGAATTTGCTCCATCTGGATCCTGTCTTTATCTCTGGCCTATTC 1140
 Db 810 TTTGGTGAACCTGCCATTCGAATTTGCTCCATCTGGATCCTGTCTTTATCTCTGGCCTATTC 869
 QY 1141 TGAAGCATTTGGCTTCTGTCATGTTGACCTTTTGAATATAGGGGTGAACAGCAATAAACCTG 1200
 Db 870 TGAAGCATTTGGCTTCTGTCATGTTGACCTTTTGAATATAGGGGTGAACAGCAATAAACCTG 929
 QY 1201 TATGCTCAATGCCACATCAAAATTTATGAGTGTCTTACCAAGATGTAAAGGACTGGTGGCT 1260
 Db 930 TATGCTCAATGCCACATCAAAATTTATGAGTGTCTTACCAAGATGTAAAGGACTGGTGGCT 989
 QY 1261 CTTCCGGGTTCTATTTCTGTATGCTTGGTGTGACCTGGTGTGACCTTCTTACACCTTCATGAC 1320

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Db 210 CAGATGGAACCCCTTGGCTCAGGCATCCTTTGGCTGGCACTGGTTGGATGTGTAAT 269
QY 541 CAGTGAATACTCTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCCACCAC 600
Db 270 CAGTGAATACTCTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTCCACCAC 329
QY 601 TTTTCGTGGCAGAGAGCTCAGCTTCTCTGTTTACCACTATCAACCCCACTAATTTGGPCT 660
Db 330 TTTTCGTGGCAGAGAGCTCAGCTTCTCTGTTTACCACTATCAACCCCACTAATTTGGPCT 389
QY 661 ACCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGCACTAAAATTTACTTCAGCTTT 720
Db 390 ACCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGCACTAAAATTTACTTCAGCTTT 449
QY 721 CAAATACATTAACACATGTGATATCTTGTACTATTTTTCATCGTGGGAATGGTGGGAATGC 780
Db 450 CAAATACATTAACACATGTGATATCTTGTACTATTTTTCATCGTGGGAATGGTGGGAATGC 509
QY 781 AACTCTGCTCAGATCATTTACAGAAACAAATGTATGAGGAATGGCCCAACCGCTGAT 840
Db 510 AACTCTGCTCAGATCATTTACAGAAACAAATGTATGAGGAATGGCCCAACCGCTGAT 569
QY 841 AGCCAGCTTGGCCCTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTATT 900
Db 570 AGCCAGCTTGGCCCTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTATT 629
QY 901 TAAGCTGCTGGCTGGCGCTGGCTTTTGATCAACAATGACTTTGGCGTATTTCTTGCAC 960
Db 630 TAAGCTGCTGGCTGGCGCTGGCTTTTGATCAACAATGACTTTGGCGTATTTCTTGCAC 689
QY 961 GCTGTTCCCTTTTGCAGAACTCTCGGTGGGGATCAACGCTCCTCAACCTCTGCGCTCT 1020
Db 690 GCTGTTCCCTTTTGCAGAACTCTCGGTGGGGATCAACGCTCCTCAACCTCTGCGCTCT 749
QY 1021 TAGTGTGACAGGTACAGAGCAGTTGCCCTCGGTGGAGTGTGTTGAGGGAATGGGATTC 1080
Db 750 TAGTGTGACAGGTACAGAGCAGTTGCCCTCGGTGGAGTGTGTTGAGGGAATGGGATTC 809
QY 1081 TTTGTTAACTGCCATGAAATGTCTCCATCTGGATCTGCTCTTTATCCTGCCATTC 1140
Db 810 TTTGTTAACTGCCATGAAATGTCTCCATCTGGATCTGCTCTTTATCCTGCCATTC 869
QY 1141 TGAAGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGTGAACAGCATAAACCTG 1200
Db 870 TGAAGCGATTGGCTTCGTCATGGTACCCCTTGAATATAGGGTGAACAGCATAAACCTG 929
QY 1201 TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAAGGACTGGTGGCT 1260
Db 930 TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAAGGACTGGTGGCT 989
QY 1261 CTTCCGGTTCTATTTCTGTATGCCCTTGGTGTGCATCGCATCTCTACACCCCTCATGAC 1320
Db 990 CTTCCGGTTCTATTTCTGTATGCCCTTGGTGTGCATCGCATCTCTACACCCCTCATGAC 1049
QY 1321 TTGTGAGATGTTGAACAGAAGAAATGGCAGCTTGAGAAATGGCCTCAGTGAACATCTTAA 1380
Db 1050 TTGTGAGATGTTGAACAGAAGAAATGGCAGCTTGAGAAATGGCCTCAGTGAACATCTTAA 1109
QY 1381 GCAGCGTCGAGAAGTGGCAAAACAGTTTCTGCTGGTGTGTAATTTTCTCTTTTGGCTG 1440
Db 1110 GCAGCGTCGAGAAGTGGCAAAACAGTTTCTGCTGGTGTGTAATTTTCTCTTTTGGCTG 1169
QY 1441 GTTCCCTCTTCACTTAAGCCGTATTTGAAGAAACTGTGTATACGAAATGGACAAGAA 1500
Db 1170 GTTCCCTCTTCACTTAAGCCGTATTTGAAGAAACTGTGTATACGAAATGGACAAGAA 1229
QY 1501 CCGATGTCATTTACTTTCTTACTCTCATGATACATCGGTATTAATTTGCGCAC 1560
Db 1230 CCGATGTCATTTACTTTCTTACTCTCATGATACATCGGTATTAATTTGCGCAC 1289
QY 1561 CATGAATTCATGTATAAACCCTCATAGCTCTGTATTTTGTGACGAAGAAATTTAAAAATG 1620
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Db 1290 CATGAATTCATGTATAAACCCTCATAGCTCTGTATTTTGTGACAAAGAAATTTAAAAATG 1349
QY 1621 TTTCCAGTCATGCTCTGCTGCTGTACAGTCCAAAAGTCTGATGACCTCGGTCC 1680
Db 1350 TTTCCAGTCATGCTCTGCTGCTGTACAGTCCAAAAGTCTGATGACCTCGGTCC 1409
QY 1681 CATGAACGGAACAAAGCATCCAGTGGAGAACACGATCAAAACCAACCAACACAGACCG 1740
Db 1410 CATGAACGGAACAAAGCATCCAGTGGAGAACACGATCAAAACCAACCAACACAGACCG 1469
QY 1741 GAGCAGCATTAAGCAGACATGAATGACACCCCTTTAGAAGCACTCTCGGTACTCCCAT 1800
Db 1470 GAGCAGCATTAAGCAGACATGAATGACACCCCTTTAGAAGCACTCTCGGTACTCCCAT 1529
QY 1801 AATCCTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC 1860
Db 1530 AATCCTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC 1589
QY 1861 CTTCTTCTTAAATTCACCTCCACACACCAAGAAAGAAATCTTTCCAAAACCGCAA -GGTAG 1919
Db 1590 CTTCTTCTTAAATTCACCTCCACACACCAAGAAAGAAATCTTTCCAAAACCGCAAAGGTAG 1649
QY 1920 ACTGGTTTATCCACCCCAACATCTACGAATCGTACTTCTTTAATTTGATCTAAATTTACAT 1979
Db 1650 ACTGGTTTATCCACCCCAACATCTACGAATCGTACTTCTTTAATTTGATCTAAATTTACAT 1709
QY 1980 ATTCTGCTGTGTTATTTCAGCAGCTTAAATAATGGTGGAGCTGGGGGAGAATGAAGACTGT 2039
Db 1710 ATTCTGCTGTGTTATTTCAGCAGCTTAAATAATGGTGGAGCTGGGGGAGAATGAAGACTGT 1769
QY 2040 TAAATGAACACAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 2099
Db 1770 TAAATGAACACAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 1829
QY 2100 GCTAGCTTTTATGSCAGTTCTGGTGAATGTTCATGGAACCTGGTACCATTGAACTTTA 2159
Db 1830 GCTAGCTTTTATGSCAGTTCTGGTGAATGTTCATGGAACCTGGTACCATTGAACTTTA 1889
QY 2160 GAGATTAACACAGAGATTTTCTACTTTTAAAGTGA -TTTTTTTGTCTTCAGCCAAACA 2218
Db 1890 GAGATTAACACAGAGATTTTCTACTTTTAAAGTGAATTTTGTCTTCAGCCAAACA 1949
QY 2219 CAATATGGGCTCAGGTCACTTTTATTTGAATGTCAATTTGGTGCCAGTAT 2268
Db 1950 CAATATGGGCTCAGGTCACTTTTATTTGAATGTCAATTTGGTGCCAGTAT 1999

RESULT 12

AAF21447
ID AAF21447 standard; DNA; 5036 BP.

AC AAF21447;

XX AAF21447;
XX 14-MAR-2001 (first entry)

XX Human endothelin receptor A polynucleotide fragment #3014.

DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

OS Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000NO-US08020.
 XX 06-APR-1999; 99US-0127958.
 XX (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 XX Nyce JW;
 XX WPI; 2000-679539/66.
 XX Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -
 XX Disclosure; Page 243-244; 1592pp; English.
 XX The present invention describes low adenosine (A) content antisense
 XX oligonucleotides and compositions (I) comprising them. In the antisense
 XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
 XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 XX The antisense oligonucleotides and (I) can be used to down-regulate the
 XX expression and or activity of target polypeptides associated with
 XX lung/respiratory disorders and malignancies, such as stimulating and
 XX activating peptide factors and transmitters, transcription factors,
 XX immunoglobulins and antibodies, antibody receptors, cytokines and
 XX chemokines, endogenously produced specific and non-specific enzymes,
 XX binding proteins, adhesion molecules and their receptors, cytokine and
 XX chemokine receptors, adenosine receptors, bradykinin receptors, central
 XX nervous system (CNS) and peripheral nervous and non-nervous system
 XX receptors, CNS and peripheral nervous and non-nervous system peptide
 XX transmitters, defensins, growth factors, vasoactive peptides and
 XX receptors, binding proteins and malignancy associated proteins. The
 XX antisense oligonucleotides may be used in this way to treat disorders
 XX including respiratory obstruction (especially pulmonary obstruction
 XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 XX and/or surfactant hypoproduction which are associated with a disease or
 XX condition selected from pulmonary vasoconstriction, inflammation,
 XX allergies, asthma, impeded respiration, respiratory distress syndrome
 XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
 XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 XX fragments and antisense oligonucleotides used in the exemplification of
 XX the present invention.
 XX Sequence 5036 BP; 1359 A; 1148 C; 1060 G; 1469 T; 0 other;
 XX Query Match 44.3%; Score 1819.6; DB 21; Length 5036;
 XX Best Local Similarity 99.7%; Pred. No. 0;
 XX Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 QY 421 AAAAGTGAAGGTGTAAGACAGACAGCAAGTGCATATAGAGATATTCCTCAAAATTTGCCT 480
 DB 1310 AAAAGTGAAGGTGTAAGACAGACAGCAAGTGCATATAGAGATATTCCTCAAAATTTGCCT 1369
 QY 481 CAAGATGGAACCTTTGCTCAGGGCATCCTTTGGCTGGCATGCTGGATGCTGAAT 540
 DB 1370 CAAGATGGAACCTTTGCTCAGGGCATCCTTTGGCTGGCATGCTGGATGCTGAAT 1429
 QY 541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTTCAACCAC 600
 DB 1430 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTTCAACCAC 1489
 QY 601 TTTTGTGGCAGAGCTCAGCTTCCTGGTTACACATCATCAACCCACTAATTTGGTCCCT 660
 DB 1490 TTTTGTGGCAGAGCTCAGCTTCCTGGTTACACATCATCAACCCACTAATTTGGTCCCT 1549
 QY 661 ACCAGCAATGGCTCAATGACACACTATTGCCACAGCAGACTAAATTTACTTCAGCTTT 720
 DB 1550 ACCAGCAATGGCTCAATGACACACTATTGCCACAGCAGACTAAATTTACTTCAGCTTT 1609

QY 721 CAAATACATTAACTGTGATATCTTGTACTATTTTTCATCGTGGAAATGGTGGGAATGC 780
 DB 1610 CAAATACATTAACTGTGATATCTTGTACTATTTTTCATCGTGGAAATGGTGGGAATGC 1669
 QY 781 AACTCTGCTCAGGATCATTTTACCAGACAAATATGATAGGAATGCCCAAGCCGCTGAT 840
 DB 1670 AACTCTGCTCAGGATCATTTTACCAGACAAATATGATAGGAATGCCCAAGCCGCTGAT 1729
 QY 841 AGCCAGTCTTGCCTTGGAGACCTTATCTATGTGTGATGATCTCCCTATCAATGTATT 900
 DB 1730 AGCCAGTCTTGCCTTGGAGACCTTATCTATGTGTGATGATCTCCCTATCAATGTATT 1789
 QY 901 TAAGCTGCTGCTGGGGCTGGCCCTTTTGTATCACAATGACTTTGGCGTATTTCTTTGCAA 960
 DB 1790 TAAGCTGCTGCTGGGGCTGGCCCTTTTGTATCACAATGACTTTGGCGTATTTCTTTGCAA 1849
 QY 961 GCTGTTCCCTTTTTCAGAGAGTCTCGTGGGGATCACCGTCTCAACCTCTGCGCTCT 1020
 DB 1850 GCTGTTCCCTTTTTCAGAGAGTCTCGTGGGGATCACCGTCTCAACCTCTGCGCTCT 1909
 QY 1021 TAGTGTTCACAGGTACAGAGCAGTTGCCCTCCTGGAGTCTGTTCAGGAAATTTGGGATTC 1080
 DB 1910 TAGTGTTCACAGGTACAGAGCAGTTGCCCTCCTGGAGTCTGTTCAGGAAATTTGGGATTC 1969
 QY 1081 TTTGGTAACCTGCCATTGAAATTTGTCTCCATCTGGAATCTGTCTTTATCTTCCCTGGCATTC 1140
 DB 1970 TTTGGTAACCTGCCATTGAAATTTGTCTCCATCTGGAATCTGTCTTTATCTTCCCTGGCATTC 2029
 QY 1141 TGAAGCATTGGCTTGGTTCATGTTACCTTTCATATAGGGGTGAACAGCATAAAACCTG 1200
 DB 2030 TGAAGCATTGGCTTGGTTCATGTTACCTTTCATATAGGGGTGAACAGCATAAAACCTG 2089
 QY 1201 TATCTCAATCCACATCAAAATTCATGGAGTCTTCAACAGATGTAAAGGACTGTGGCT 1260
 DB 2090 TATCTCAATCCACATCAAAATTCATGGAGTCTTCAACAGATGTAAAGGACTGTGGCT 2149
 QY 1261 CTTCCGGTTCATTTCTGTATGTCCTTGGTGTGCACTCGATCTTCTACACCTCATGAC 1320
 DB 2150 CTTCCGGTTCATTTCTGTATGTCCTTGGTGTGCACTCGATCTTCTACACCTCATGAC 2209
 QY 1321 TTGTGAGATGTTGAACAGAAAGTGGCAGCTTGAGATTCGCCCTCAGTGAACATCTTAA 1380
 DB 2210 TTGTGAGATGTTGAACAGAAAGTGGCAGCTTGAGATTCGCCCTCAGTGAACATCTTAA 2269
 QY 1381 GCAGCTCGAAGTGGCAAAACAGTTTCTGCTGTTGTTGTAATTTTGTCTTTTGTGCTG 1440
 DB 2270 GCAGCTCGAAGTGGCAAAACAGTTTCTGCTGTTGTTGTAATTTTGTCTTTTGTGCTG 2329
 QY 1441 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAATATGGAACAA 1500
 DB 2330 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAATATGGAACAA 2389
 QY 1501 CCGATGTAATTAATTAAGTCTTCTACTGCTCATGATACATCGGATTAATTAATTCGCAAC 1560
 DB 2390 CCGATGTAATTAATTAAGTCTTCTACTGCTCATGATACATCGGATTAATTAATTCGCAAC 2449
 QY 1561 CATGAATTCATGTAATAAACCCTAGCTCTGTATTTTGTGAGCAAGAAATTTAAATTTG 1620
 DB 2450 CATGAATTCATGTAATAAACCCTAGCTCTGTATTTTGTGAGCAAGAAATTTAAATTTG 2509
 QY 1621 TTTCCAGTCACTGCTGCTGCTGTGTATACAGTCCAAAGTCTGTATGACCTCGGTGCC 1680
 DB 2510 TTTCCAGTCACTGCTGCTGCTGTGTATACAGTCCAAAGTCTGTATGACCTCGGTGCC 2569
 QY 1681 CATGAACGGAACAGCATCCAGTGAAGAACACCATCAAAACACACACACAGACCG 1740
 DB 2570 CATGAACGGAACAGCATCCAGTGAAGAACACCATCAAAACACACACAGACCG 2629
 QY 1741 GAGCAGCCATGAAGACAGCATGAAGTACACCTTCTAGAGCAGCTCTCGGTACTCCCAT 1800
 DB 2630 GAGCAGCCATGAAGACAGCATGAAGTACACCTTCTAGAGCAGCTCTCGGTACTCCCAT 2689

QY 1801 AATCCTCTCGGAGAAAAAATCACAAGGCACTGTGACTCGGGAATCTTCTCTGATC 1860
 Db AATCCTCTCGGAGAAAAAATCACAAGGCACTGTGACTCGGGAATCTTCTCTGATC 2749
 QY 1861 CTCTCTCTTAATTAATCACTCCACACCAAGAGAAATGCTTCCAAACCCGCA-GGTAG 1919
 Db CTCTCTCTTAATTAATCACTCCACACCAAGAGAAATGCTTCCAAACCCGCAAGGGTAG 2809
 QY 1920 ACTGGTTTATCCACCCCAACATCTCGAATCGTACTTCTTAAATGATCTAAATTTACAT 1979
 Db ACTGGTTTATCCACCCCAACATCTCGAATCGTACTTCTTAAATGATCTAAATTTACAT 2869
 QY 1980 ATTCTGGTGTGATTCAGCACTAAAAAATGTTGGGAGCTGGGGAGAAATGAAGACTGT 2039
 Db ATTCTGGTGTGATTCAGCACTAAAAAATGTTGGGAGCTGGGGAGAAATGAAGACTGT 2929
 QY 2040 TAAATGAACCAAGAGATATTTACTACTTTTGTGATGAAATAGAGCTTTCAAGTACATG 2099
 Db TAAATGAACCAAGAGATATTTACTACTTTTGTGATGAAATAGAGCTTTCAAGTACATG 2989
 QY 2100 GCTAGCTTTTATGGCAGTCTGTTGAATGTTCAATGGGAATGCTCACCATGAACCTTTA 2159
 Db GCTAGCTTTTATGGCAGTCTGTTGAATGTTCAATGGGAATGCTCACCATGAACCTTTA 3049
 QY 2160 GAGATTAACGACAGATTTTCTACTTTTTTAAGTGA-TTTTTGTCTCTCAGGCCAACA 2218
 Db GAGATTAACGACAGATTTTCTACTTTTTTAAGTGA-TTTTTGTCTCTCAGGCCAACA 3109
 QY 2219 CAATATGGGCTCAGGTCACCTTTTATTTGAATGTCATTTGGTGCCAGTAT 2268
 Db CAATATGGGCTCAGGTCACCTTTTATTTGAATGTCATTTGGTGCCAGTAT 3159

RESULT 13
 AAF21435
 ID AAF21435 standard; DNA; 117609 BP.
 XX AC AAF21435;
 XX AC AAF21435;
 DT 14-MAR-2001 (first entry)
 XX Human receptor-related antisense polynucleotide #3002.
 DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 W respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 XX OS
 XX W0200062736-A2.
 XX PN
 XX 26-OCT-2000.
 XX PD
 XX 24-MAR-2000; 2000MO-US08020.
 XX PF
 XX 06-APR-1999; 99US-0127958.
 XX PR
 XX (UYEC-) UNIV EAST CAROLINA.
 XX PA (NYCE/) NYCE J W.
 XX PI Nyce JW;
 XX NYCE J W;
 XX WPI; 2000-679539/66.
 DR Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating

Cancers and respiratory obstructions -

Disclosure; Page 17-47; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

XX SQ Sequence 117609 BP; 27530 A; 29942 C; 30320 G; 29441 T; 376 other;

Query Match

Best Local Similarity 44.3%; Score 1819.6; DB 21; Length 117609;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 421 AAAAGTGAAGGTGTAAGAGCAGCACAAGTGCATTAAGAGATATTTCCTCAAAATTTGCCT 480
 Db 87367 AAAAGTGAAGGTGTAAGAGCAGCACAAGTGCATTAAGAGATATTTCCTCAAAATTTGCCT 87426
 QY 481 CAAGATGAARACCTTTGCCTCAGGCATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 540
 Db 87427 CAAGATGAARACCTTTGCCTCAGGCATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 87486
 QY 541 CAGTATATCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCCACCAC 600
 Db 87487 CAGTATATCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCCACCAC 87546
 QY 601 TTTTGGTGCCAGAGCTCAGCTTCCCTGTACCTATCATCAACCACCTAAATTTGGTCT 660
 Db 87547 TTTTGGTGCCAGAGCTCAGCTTCCCTGTACCTATCATCAACCACCTAAATTTGGTCT 87606
 QY 661 ACCAGCAATGGCTCAATGCCACAATATTTGCCAGCAGACTATAATTTACTTCAGCTTT 720
 Db 87607 ACCAGCAATGGCTCAATGCCACAATATTTGCCAGCAGACTATAATTTACTTCAGCTTT 87666
 QY 721 CAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC 780
 Db 87667 CAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGC 87726
 QY 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGCTGAT 840
 Db 87727 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGCTGAT 87786
 QY 841 AGCCAGTCTTGGCTTGGAGACCTTATCTATGTGTCATTTGATCTCCCTATCAATGATTT 900
 Db 87787 AGCCAGTCTTGGCTTGGAGACCTTATCTATGTGTCATTTGATCTCCCTATCAATGATTT 87846
 QY 901 TAAGCTGTGCTGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTCTTTTGCAA 960

Db	87847	TAAGCTGCTGGCTGGCGCTGGCCCTTTTGATCACAAATGACATTGGCGTATTTCCTTTGGCAA	87906
Qy	961	GCTGTTCCCTTTTGTGCAGAGTCTCCGTTGGGATCACCCTCCTCAACCTCTGGCGTCT	1020
Db	87907	GCTGTTCCCTTTTGTGCAGAGTCTCCGTTGGGATCACCCTCCTCAACCTCTGGCGTCT	87966
Qy	1021	TAGTGTTCACAGGTACAGAGCAGTTGGCTCCTGGAGTCTGTTTCAGGGAATTTGGGATGCC	1080
Db	87967	TAGTGTTCACAGGTACAGAGCAGTTGGCTCCTGGAGTCTGTTTCAGGGAATTTGGGATGCC	88026
Qy	1081	TTTGGTAACTGCCAATTGAAATTTGCTCCATCTGGATCCTGCTTATCTTATCTTGGCCATTGCC	1140
Db	88027	TTTGGTAACTGCCAATTGAAATTTGCTCCATCTGGATCCTGCTTATCTTATCTTGGCCATTGCC	88086
Qy	1141	TGAAGCGAATTTGGCTTCGTCATGTTACCTTTTGAATATAGGGGTGAACAGCATATAAACCTG	1200
Db	88087	TGAAGCGAATTTGGCTTCGTCATGTTACCTTTTGAATATAGGGGTGAACAGCATATAAACCTG	88146
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTCTCTACCAAGATCTAAAGGACTGGTGGCT	1260
Db	88147	TATGCTCAATGCCACATCAAAATTCATGGAGTCTCTACCAAGATCTAAAGGACTGGTGGCT	88206
Qy	1261	CTTCCGGTTCTATTCTTGATATGCCCCCTTGGTGTGCACATGCGATCTCTACACCCCTCATGAC	1320
Db	88207	CTTCCGGTTCTATTCTTGATATGCCCCCTTGGTGTGCACATGCGATCTCTACACCCCTCATGAC	88266
Qy	1321	TTGTGAGATGTTGAACAGAGGAATGTCAGCTTCAGAAATTCCTCATGTCAGTGAACATCTTAA	1380
Db	88267	TTGTGAGATGTTGAACAGAGGAATGTCAGCTTCAGAAATTCCTCATGTCAGTGAACATCTTAA	88326
Qy	1381	GCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	88327	GCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTGGTTGTAATTTTGGCTCTTTGCTG	88386
Qy	1441	GTTCCTCTTCACATTAGCCGTATATTGAGAAACATCTGTATAACGAAATGGACAAGAA	1500
Db	88387	GTTCCTCTTCACATTAGCCGTATATTGAGAAACATCTGTATAACGAGATGGACAAGAA	88446
Qy	1501	CCGATGTGAATTACTTAAGTTCTTACTGCATGCTACATCGGATTAACATTTGGCAAC	1560
Db	88447	CCGATGTGAATTACTTAAGTTCTTACTGCATGCTACATCGGATTAACATTTGGCAAC	88506
Qy	1561	CATGAATTCATGATATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	88507	CATGAATTCATGATATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	88566
Qy	1621	TTTCCAGTCATGCTCTGCTGCTGTACCAAGTCCAAAGTCTGATGACCTCGGTPCC	1680
Db	88567	TTTCCAGTCATGCTCTGCTGCTGTACCAAGTCCAAAGTCTGATGACCTCGGTPCC	88626
Qy	1681	CATGAACGGAACCAAGCATCCAGTGGGAAGAACCCAGATCAAAACCAACCAACAGACCG	1740
Db	88627	CATGAACGGAACCAAGCATCCAGTGGGAAGAACCCAGATCAAAACCAACCAACAGACCG	88686
Qy	1741	GAGCAGCCATAAGCAGCAGATGAACATGACACCCCTTAGAGACTCTCTCGGTACTCCCAT	1800
Db	88687	GAGCAGCCATAAGCAGCAGATGAACATGACACCCCTTAGAGACTCTCTCGGTACTCCCAT	88746
Qy	1801	AATPCTCTCGGAGAAAAAATCACAGGCAACTGTCACTCCGGGAATCTCTCTCTGATC	1860
Db	88747	AATPCTCTCGGAGAAAAAATCACAGGCAACTGTCACTCCGGGAATCTCTCTCTGATC	88806
Qy	1861	CTTCTTCTTAATTCACTCCACACCAAGAAATGCTTTTCCAAAACCGCAA -GGTAG	1919
Db	88807	CTTCTTCTTAATTCACTCCACACCAAGAAATGCTTTTCCAAAACCGCAAGGCTAG	88866
Qy	1920	ACTGGTTTATCCACCACCAACATCTACGAATCGTACTCTTTTAATTTGATCTAATTTACAT	1979
Db	88867	ACTGGTTTATCCACCACCAACATCTACGAATCGTACTCTTTTAATTTGATCTAATTTACAT	88926
Qy	1980	ATTCTCGGTGTGTTATTCAGCAGCTAAAAAATGGTGGGAGATGAAGACTGT	2039

Db	88927	ATTCTCGCTGTTCTATT	CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATCAAGACTGT	88988
Qy	2040	TAATATCAAAACCAAGAGATATT	TACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG	2099
Db	88987	TAATATCAAAACCAAGAGATATT	TACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG	89046
Qy	2100	GCTAGCTTTTATGGCAGTCTCT	GGTGAATGTTCAATGGGAACCTGGTCAACCATGAAACTTTTA	2159
Db	89047	GCTAGCTTTTATGGCAGTCTCT	GGTGAATGTTCAATGGGAACCTGGTCAACCATGAAACTTTTA	89106
Qy	2160	GAGATTACGACACAGATTTCT	TACTTTTTTAAAGTGA-TTTTTGTCTCTCAGCCAAACA	2218
Db	89107	GAGATTACGACACAGATTTCT	TACTTTTTTAAAGTGAATTTTTTGTCTCTCAGCCAAACA	89166
Qy	2219	CAATATGGGCTCAGTCACTTTT	TATTTCAATGTCATTTGGTGGCCAGTAT	2268
Db	89167	CAATATGGGCTCAGTCACTTTT	TATTTCAATGTCATTTGGTGGCCAGTAT	89216
RESULT	14			
ID	AAF20902			
XX	AAF20902	standard; DNA; 1310 BP.		
AC	AAF20902;			
DT	14-MAR-2001	(first entry)		
DE	Human endothelin receptor A	polynucleotide fragment #2459.		
KW	Low adenosine antisen-	se oligonucleotide; phosphorothioate; allergy;		
KW	human; airway disorder;	bronchoconstriction; lung inflammation;		
KW	surfactant depletion;	respiratory; bronchodilator; antiinflammatory;		
KW	immunosuppressive;	antialsthmic; analgesic; hypotensive; cytostatic;		
KW	respiratory obstruction;	pulmonary obstruction; impeded respiration;		
KW	resurfactant hypoproduction;	pulmonary vasoconstriction; asthma; RDS;		
KW	respiratory distress syndrome;	pain; cystic fibrosis; allergic rhinitis;		
KW	pulmonary hypertension;	emphysema; pulmonary transplantation rejection;		
KW	chronic obstructive pulmonary	disease; pulmonary infection; bronchitis;		
KW	cancer; ss.			
XX	XX			
OS	Homio sapiens.			
XX	XX			
PN	WO200062736-A2.			
XX	XX			
PD	26-OCT-2000.			
XX	XX			
PF	24-MAR-2000; 2000WO-US08020.			
XX	XX			
PR	06-APR-1999; 99US-0127958.			
XX	XX			
PA	(UYEC-) UNIV EAST CAROLINA.			
PA	(NYCE/) NYCE J W.			
XX	XX			
PI	Nyce JW;			
XX	XX			
DR	WPI; 2000-679539/66.			
XX	XX			
PT	Low adenosine (A) content	antisense oligonucleotides which do not		
PT	trigger adenosine receptors	during metabolism, useful e.g. for treating		
PT	cancers and respiratory	obstructions -		
XX	XX			
PS	Disclosure; Page 244-245;	1592pp; English.		
XX	XX			
CC	The present invention	describes low adenosine (A) content antisense		
CC	oligonucleotides and	compositions (I) comprising them. In the antisense		
CC	oligonucleotides the A	is replaced by a 'Universal' or alternative base.		
CC	(I) can have respiratory,	bronchodilator, antiinflammatory, analgesic,		
CC	immunosuppressive,	antialsthmic, hypotensive and cytostatic activities.		
CC	The antisense oligonucle-	otides and (I) can be used to down-regulate the		
CC	expression and or activity	of target polypeptides associated with		
CC	lung/respiratory disorders	and malignancies, such as stimulating and		
CC	activating peptide factors	and transmitters, transcription factors,		
CC	immunoglobulins and anti-	bodies, antibody receptors, cytokines and		

(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 177-178; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1310 BP; 337 A; 312 C; 284 G; 377 T; 0 other;

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Query Match          31.6%; Score 1296.8; DB 21; Length 1310;
Best Local Similarity 99.5%; Pred. No. 1.7e-303;
Matches 1301; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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481 CAAGATGGAAACCCCTTGGCTCAGGGCATCCTTTGGCTGGCAGCTGTTGGATGTGTAAT 540
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 3 CACCATGGAAACCCCTTGGCTCAGGGCATCCTTTGGCTGGCAGCTGTTGGATGTGTAAT 62

541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAAATCATGTGGATGATTTCACCAC 600

63 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACCAC 122

601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTGGTCCT 660

b 123 TTTTCGTGGCACAGAGCTCAGCTTCCCTGGTTACCACTCATCAACCCACTAAATTGGTCCT 182

661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAAATTACTTCAGCCTT 720

183 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT 242

721 CAAATACATTAACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC 780

243 CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC 302

781 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGGCTGAT 840

303 AACTCTGCTCAGGATCATTTACCAGAACAATAATGTATGAGGAATGGCCCAACGGCGTGAT 362

Qy	841	AGCCAGTCTTGGCCCTTGGAGACCTTATCATGTGTGTCATTTGATCTCCCTATCAATGTATT	900
Db	363	AGCAAGTCTTGGCCCTTGGAGACCTTATCTATGTGTCATTTGATCTCCCTATCAATGTATT	422
Qy	901	TAGCTGCTGGCTGGCGCTGGCCCTTTTGATCACAATGACITTTGGCGTATTTCTTTGCCAA	960
Db	423	TAGCTGCTGGCTGGCGCTGGCCCTTTTGATCACAATGACITTTGGCGTATTTCTTTGCCAA	482
Qy	961	GCTGTTCCCTTTTTCAGAAAGTCTCGGTGGGGATCACCGTCTCAACCTCTCGCGTCT	1020
Db	483	GCTGTTCCCTTTTTCAGAAAGTCTCGGTGGGGATCACCGTCTCAACCTCTCGCGTCT	542
Qy	1021	TAGTGTGACAGTACAGAGCAGTGTCCCTCTGAGTCTGTGTACAGGAATTTGGATTC	1080
Db	543	TAGTGTGACAGGTACAGAGCAGTGTCCCTCTGAGTCTGTGTACAGGAATTTGGATTC	602
Qy	1081	TTTGGTAACTGCCATTGAAATTTGCTCCATCTGGATCTGTCTTTATCCTGGCCATTC	1140
Db	603	TTTGGTAACTGCCATTGAAATTTGCTCCATCTGGATCTGTCTTTATCCTGGCCATTC	662
Qy	1141	TGAAGCGATTGGCTTCGTCATCGTACCCCTTTTGAATATAGGGGTGAACAGCAATAAACCTG	1200
Db	663	TGAAGCGATTGGCTTCGTCATCGTACCCCTTTTGAATATAGGGGTGAACAGCAATAAACCTG	722
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGAGTCTTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	723	TATGCTCAATGCCACATCAAAATTCATGAGTCTTACCAAGATGTAAAGGACTGGTGGCT	782
Qy	1261	CTTCCGGTCTATTCTCTGTATGCCCTTGGTGTGCACTCGGATCTCTACACCCCTCATGAC	1320
Db	783	CTTCCGGTCTATTCTCTGTATGCCCTTGGTGTGCACTCGGATCTCTACACCCCTCATGAC	842
Qy	1321	TTCTGAGATCTTGAACAGAAGGAATGGCAGCTTGAAGATTCGCCCTCAGTGAACATCTTAA	1380
Db	843	TGCTGAGATCTTGAACAGAAGGAATGGCAGCTTGAAGATTCGCCCTCAGTGAACATCTTAA	902
Qy	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTTCGTGTGGTGTGTAAATTTTGTCTTTGCTG	1440
Db	903	GCAGCGTCGAGAAGTGGCAAAACAGTTTTTCGTGTGGTGTGTAAATTTTGTCTTTGCTG	962
Qy	1441	GTTCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATACGAAATGGACAAGAA	1500
Db	963	GTTCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATACGAAATGGACAAGAA	1022
Qy	1501	CCGATGTGAATTAATTAGTPTTCTTACTGCTCATGGATTTACATCGGTATTAACCTTGGCAAC	1560
Db	1023	CCGATGTGAATTAATTAGTPTTCTTACTGCTCATGGATTTACATCGGTATTAACCTTGGCAAC	1082
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1083	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1142
Qy	1621	TTTCCAGTCATGCTCTGCTGCTGTGTATACAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1143	TTTCCAGTCATGCTCTGCTGCTGTGTATACAGTCCAAAAGTCTGATGACCTCGGTCCC	1202
Qy	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACCCAGATCAAAACCAACCAACACAGACCG	1740
Db	1203	CATGAACGGAACAAGCATCCAGTGGGAAGAACCCAGATCAAAACCAACCAACACAGACCG	1262
Qy	1741	GAGCAGCCATTAAGGACAGCATGAATGACACCCCTTAGAAGCACTCCT	1788
Db	1263	GAGCAGCCATTAAGGACAGCATGAATGACACCCCTTAGAAGCACTCCT	1310

Search completed: December 12, 2002, 10:21:31
Job time : 1222 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:25:42 ; Search time 10083 Seconds
(without alignments)
11848.360 Million cell updates/sec

Title: US-09-931-157-1

Perfect score: 4105

Sequence: 1 gaattcggcgccgtcttg.....taaaagtacagaaacctt 4105

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

arched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4105	100.0	4105	6	AR177879 Sequence
2	4105	100.0	4105	6	E07649 cDNA encodi
3	4105	100.0	4105	9	X61950 H.sapiens m
4	4103	100.0	4105	9	S57498 endothelein
5	4101	99.9	4101	9	D90348 Human mRNA
6	3183.2	77.5	3305	9	S45956 endothelein
7	2609.6	63.6	2705	9	BC022511 Homo sapi
8	2470	60.2	2595	9	D11511 Human DNA f
9	2409.2	58.7	164920	9	AC093908 Homo sapi
10	2292	55.8	2337	11	G06463 human STS W
11	1819.6	44.3	1868	9	S63938 A-type endo
12	1786.6	43.5	3216	4	BTBETREC Bovine mRNA
13	1560.2	38.0	1661	9	S67127 endothelein
14	1359	33.1	1359	9	S81539 endothelein-
15	1296.8	31.6	1310	9	L06622 Homo sapien
16	1280.8	31.2	1284	6	AX280871 Sequence
17	1122	27.3	1374	4	S80652 endothelein
18	1103.2	26.9	1284	4	AF416703 Ovis arie
19	1088.2	26.5	2696	10	BC008277 Mus muscu
20	1048.8	25.5	1180	4	AF311974 Oryctolag
21	1021	24.9	1021	11	G10643 human STS C
22	997	24.3	1436	10	RATENDOR Rat endothe
23	951	23.2	1160	9	S81542 endothelein-
24	765.8	18.7	2944	5	AF040634 Gallus ga
25	765.8	18.7	2988	5	AF472618 Gallus ga
26	695	16.9	1032	9	S81545 endothelein-
27	632.8	15.4	1650	5	XL006633 Xenopus lae
28	624.6	15.2	810	10	AF039892 Mus muscu
29	514	12.5	530	9	MF020577 Macaca fasc
30	492.4	12.0	531	9	HUMETAR2 Human DNA f
31	487.4	11.9	1435	9	S55547S2 ETA=endothe
32	487.4	11.9	66264	2	AC110065 Homo sapi
33	425	10.4	1308	5	CCEDNRB2 Coturnix co
34	423.4	10.3	2225	5	AF472617 Gallus ga
35	411.6	10.0	1724	5	AB045356 Oryzias l
36	411	10.0	1314	4	AF276427 Canis fam
37	407.8	9.9	1311	4	AF038900 Equus cab
38	407.8	9.9	1452	4	AF034530 Canis fam
39	406.2	9.9	1321	6	AR207426 Sequence
40	403.8	9.8	1892	10	RNETBREC Rat mRNA fo
41	403.8	9.8	1965	6	E03623 DNA encodin
42	403.8	9.8	2018	10	S65355 nonselectiv
43	403	9.8	1326	4	AF245469 Oryctolag
44	403	9.8	1669	4	AF019072 Equus cab
45	402.4	9.8	1564	5	AF472616 Gallus ga

ALIGNMENTS

RESULT 1
AR177879

LOCUS

DEFINITION

AR177879

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AR177879

Sequence

1 from patent US 6313276.

AR177879

AR177879.1

GI:17920234

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 4105)

Imura, H., Nakao, K. and Nakanishi, S.

Human endothelein receptor

Patent: US 6313276-A 1 06-NOV-2001;

Location/Qualifiers

linear

DNA

4105 bp

PAT 17-DEC-2001

[illegible]

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Qy	2101	CTAGCTTTTATGCGACTTCTGCTGAATGTTCAATGGGAACGGTCAACCATGAACATTTAG	2160
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Db	2761	ATGATTCGGAATTTTCATTTCAGGTATTTGTAATAGTCACATATATATGATATACATAT	2820
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Db	3121	AAAACTCTTTTACTAGTGTGTGTGTGTATATATAAACAATTCGTAATTTCTTTTTAGCC	3180
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Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTCACAAATGGGATATA	3420
Qy	3421	AGAGCAGCGTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTTTGGTTGGT	3480
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RESULT 2
E07649
LOCUS
DEFINITION
ACCESSION
VERSION

E07649 ·4105 bp RNA linear PAT 29-SEP-1997
cDNA encoding endothelin receptor, ETA-receptor.

E07649
E07649.1 GI:2175784

JP 1994157595-A/1.
SOURCE Homo sapiens.
-ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4105)
AUTHORS Imura,H., Nakao,I. and Nakanishi,S.
TITLE HUMAN ENDOTHELIN RECEPTOR
JOURNAL Patent: JP 1994157595-A 1 03-JUN-1994;
SHIONOGI & CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1994157595-A/1
PD 03-JUN-1994
PF 12-JUL-1991 JP 1991172828
PI IMURA HIROO, NAKAO IKIRAZU, NAKANISHI SHIGETADA PC
C07K13/00,C12N5/10,C12N15/12,C12P21/02,C12N5/10,C12R1:91), PC
(C12P21/02,
PC C12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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IDS# 5

RESULT 3
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LOCUS H. sapiens mRNA for endothelin-1 receptor.
DEFINITION X61950
ACCESSION X61950
VERSION X61950.1 GI:288312
KEYWORDS endothelin-1 receptor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4105)
Hosoda, K., Nakao, K., Hiroshi-Arai, Suga, S., Ogawa, Y., Mukoyama, M.,
Shirakami, G., Saito, Y., Nakanishi, S. and Imura, H.
Cloning and expression of human endothelin-1 receptor cDNA
FEBS Lett. 287 (1-2), 23-26 (1991)
91348221
PUBMED 1652463

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Arai, H., Nakao, K., Hosoda, K., Ogawa, Y., Nakagawa, O., Komatsu, Y. and
Imura, H.
Molecular cloning of human endothelein receptors and their
expression in vascular endothelial cells and smooth muscle cells
Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)
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PUBMED 1291713
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entry [NCBI gibbsq 128422] from the original journal article.
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 Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.
 Cloning and expression of human endothelin-1 receptor cDNA
 FEBS Lett. 287 (1-2), 23-26 (1991)
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 COMMENT These data kindly submitted in computer readable form by: kazuwa Nakao
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 Kyoto University School of Medicine
 54 Shogoin Kawahara-cho
 Sakyo-ku, Kyoto 606
 Japan
 Phone: 075-751-3170
 Fax: 075-771-9452
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DB	1621	CAGTCATGCTCTGCTGCTGTGTATACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG	1680
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[illegible]

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ACCESSION S45956
VERSION S45956.1 GI:257375
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3305)
AUTHORS Hayzer, D.J., Rose, P.M., Lynch, J.S., Webb, M.L., Kienzle, B.K.,
Liu, E.C., Bogosian, E.A., Brinson, E. and Runge, M.S.

TITLE Cloning and expression of a human endothelin receptor: subtype A
JOURNAL Am. J. Med. Sci. 304 (4), 231-238 (1992)
MEDLINE 93035452
PUBMED 1415318
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115436] from the original journal article.
This sequence comes from Fig. 2.

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ORIGIN

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VERSION BC022511.1 GI:18490297
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2705)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, J., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 32 Row: j Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503464.

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ORIGIN

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DB	121	AGTTTCTGAAGCGGGGAAGCTGTGACGCGGAGCCGCCCGCGCGGAGCCGGAC	180				
QY	314	ACCGGCCACCCCTCCGCGGCCACCCCTCGCTTCTCCGGCTTCTCTGCGCCAGCGGCC	373				
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HUMETAR8			

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  VERSION     AC093908.3 GI:18497272
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  ORGANISM    Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 164920)
               Sulston, J.E. and Waterston, R.
               Toward a complete human genome sequence
               Genome Res. 8 (11), 1097-1108 (1998)
               99063792
               9847074
               2 (bases 1 to 164920)
               Paulson, E., Cotton, M. and Creason, K.
               The sequence of Homo sapiens BAC clone RP11-752L20
               Unpublished (2001)
               3 (bases 1 to 164920)
               Waterston, R.H.
               Direct Submission
               Submitted (10-SEP-2001) Genome Sequencing Center, Washington
               University School of Medicine, 4444 Forest Park Parkway, St. Louis,
               MO 63108, USA
               4 (bases 1 to 164920)
               Waterston, R.H.
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               University School of Medicine, 4444 Forest Park Parkway, St. Louis,
               MO 63108, USA
               5 (bases 1 to 164920)
               Waterston, R.
               Direct Submission
               Submitted (08-FEB-2002) Department of Genetics, Washington
               University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
               6 (bases 1 to 164920)
               Waterston, R.
               Direct Submission
               Submitted (01-MAR-2002) Department of Genetics, Washington
               University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
               On Feb 5, 2002 this sequence version replaced gi:15778805.
               ----- Genome Center
               Center: Washington University Genome Sequencing Center
               Center code: WUGSC
               Web site: http://genome.wustl.edu/gsc
               Contact: sapiens@watson.wustl.edu
               ----- Summary Statistics
               Center project name: H_NH0752L20
               Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-56E3. Actual start of this clone is at base position 1 of RP11-752L20; actual end is at base position 164920 of RP11-752L20.

Data from AC083898 was used to finish this clone, AC093908.

The sequence of AC067873 has been incorporated into AC093908.

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misc_feature	7694..8060 /rpt_family="ERVL" 8064..8089 /rpt_family="(T)n" 8077..8089 /note="similar to Homo sapiens EST BG284616 (NID:gl3035741)"
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misc_feature	9302..10048 /note="similar to Homo sapiens EST BG683630 (NID:gl3915027)"
misc_feature	9423..10120 /note="similar to Homo sapiens EST BG824910 (NID:gl3915027)"

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	Best Local Similarity		99.4%;		Pred No. 0;					
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Qy	1624	COAGTCATGCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGATGACCTCGGTCCCCCAT	1683							
Db	93358	CCAGTCATGCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGATGACCTCGGTCCCCCAT	93417							
Qy	1684	GAACGGACAAGCATCCAGTGGAAAGAACCAACGATCAAAACAACACACACAGACGGAG	1743							
Db	93418	GAACGGACAAGCATCCAGTGGAAAGAACCAACGATCAAAACAACACACAGACGGAG	93477							
Qy	1744	CAGCCATAAGGACACGATGAACGTGACCAACCCCTTAGAAGCACCTCTCGGTACCTCCATAAT	1803							
Db	93478	CAGCCATAAGGACACGATGAACGTGACCAACCCCTTAGAAGCACCTCTCGGTACCTCCATAAT	93537							
Qy	1804	CCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATCTCT	1863							
Db	93538	CCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATCTCT	93597							
Qy	1864	CTTCTTTAATTCACCTCCACACCCGAAGAGAAATGCTTTTCCAAAACCGCAA--GGTAGACT	1922							
Db	93598	CTTCTTTAATTCACCTCCACACCCGAAGAGAAATGCTTTTCCAAAACCGCAAGGTAGACT	93655							
Qy	1923	GGTTTTATCCACCCACAACATCTFACCAATCGTACTTCTTTAATTGATCTAATTTACATAAT	1982							
Db	93658	GGTTTTATCCACCCACAACATCTFACCAATCGTACTTCTTTAATTGATCTAATTTACATAAT	93717							
Qy	1983	CTGCGTGTGTATTCAGCACTAAAAAATGGTGGAGCTGGGGAGAATGAAGACTGTAA	2042							
Db	93718	CTGCGTGTGTATTCAGCACTAAAAAATGGTGGAGCTGGGGAGAATGAAGACTGTAA	93777							
Qy	2043	ATGAACACAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCT	2102							
Db	93778	ATGAACACAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCT	93833							
Qy	2103	AGCTTTTATGGCAGTCTGGTGAATGTTCAATGGCACTGGTCCACCATGAACCTTTTAGAG	2162							
Db	93838	AGCTTTTATGGCAGTCTGGTGAATGTTCAATGGCACTGGTCCACCATGAACCTTTTAGAG	93897							
Qy	2163	ATTACGACAAGATTTTCTACTTTTTTTTAAAGTGA--TTTTTGTCTCTCAGCCAAAACACAA	2221							
Db	93898	ATTACGACAAGATTTTCTACTTTTTTTTAAAGTGAATTTTTTGTCTCTCAGCCAAAACACAA	93957							
Qy	2222	TATGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGGCCAGTATTTTTTAACTGCAT	2281							
Db	93958	TATGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGGCCAGTATTTTTTAACTGCAT	94017							
Qy	2282	AATAGCCTAAACATGATTATTGAACCTATTACACATAGTTTGAAAAAANAAGACAAAA	2341							
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Qy	2342	ATAGTATTCAGGTGAGCAATTAGATTAGTTTTCACGCTCACTATTATTATTTTTTAAAA	2401							
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QY 2642 AAATCAATGTCAAGTACCAAAATGTAATGTATGTGTCAATTTAACTCTGCCCTGAGACTTT 2701
Db 94377 AAATCAATGTCAAGTACCAAAATGTAATGTATGTGTCAATTTAACTCTGCCCTGAGACTTT 94436
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3362 GTAGCAACCTTCTCTCATTAATAATCTTGTAACTGTTACCATTAACAAATGGGATATAA 3421
Db 95094 GTAGCAACCTTCTCTCATTAATAATCTTGTAACTGTTACCATTAACAAATGGGATATAA 95153
QY 3422 GAGCAGCGTGAAGCAGATGAGCTGGAGTAGCAATATAGGGTTTGTGTTGGTTGGTT 3481
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QY 3482 GGTGTTGATAAGCAGTATTTGGGGTTCATATTTGTTCCCTGCTGGAGCAAAAGTCATTAC 3541
Db 95214 GGTGTTGATAAGCAGTATTTGGGGTTCATATTTGTTCCCTGCTGGAGCAAAAGTCATTAC 95273
QY 3542 ACTTTGAAGTATTAATTTGTTCTTATCTCAATTCATGTTGTTGATGAAATGGCAGGTT 3601
Db 95274 ACTTTGAAGTATTAATTTGTTCTTATCTCAATTCATGTTGTTGATGAAATGGCAGGTT 95333
QY 3602 GTCGTATATTTCTTTCAGACTTCCCGCAGACAGATTTGTTGATAATAAATAGGTAAGATAA 3661
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QY 3662 TTTGTTGGGCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTGTAATGTC 3721
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QY 3782 ATCATATGCAAGTAT 3841
Db 95514 ATCATATGCAAGTAT 95573
QY 3842 CAATGTCTTTTTCAGAGTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3901
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QY 3962 AACTGTGGTTTACTAGCAGGAATATTTCCAAATTTTACCTTTTACTACATCTTTTCAACAA 4021
Db 95694 AACTGTGGTTTACTAGCAGGAATATTTCCAAATTTTACCTTTTACTACATCTTTTCAACAA 95753
QY 4022 GTAACCTTCTAGAAATGAGCCAGAACCCAGGCCCTGAGTTGGCAGTGGCCCATTAAGTGT 4081
Db 95754 GTAACCTTCTAGAAATGAGCCAGAACCCAGGCCCTGAGTTGGCAGTGGCCCATTAAGTGT 95813
QY 4082 AAAATAAAGTTTACAGAAACCTT 4105
Db 95814 AAAATAAAGTTTACAGAAACCTT 95837

RESULT 10
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LOCUS human STS WI-7226, sequence tagged site.
DEFINITION G06463
ACCESSION G06463
VERSION G06463.1 GI:859708
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STS derived from sequences in dbEST and the Unigene collection.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2337)
AUTHORS Hudson, T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GATCGAATTTTTCAGATGATTCG
Primer B: AAATGCCAGCAAAAGTCAC
STS size: 343
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from D90348 -- Unigene.

Location/Qualifiers
1. .2337

/organism="Homo sapiens"

/db xref="taxon:9606"

/map="713_C_7; 722_B_3; 744_F_5; 933_G_4; 950_A_4;

827_H_10"

978. .1320

978. .1000

primer_bind complement(1301. .1320)

primer_bind 694 a 407 c 407 g 784 t 45 others

--ORIGIN

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QY 1829	CAACTGTGACTCCGGGATCTCTCTGATCCTCTCTCTTAATCTCCACACCA 1888		
Db 61	CAACTGTGACTCCGGGATCTCTCTGATCCTCTCTCTTAATCTCACTCCACACCA 120		
QY 1889	AGAAGAAATGCTTCCAAAACCGCAAGTAGACTGGTTATCCACCCACAACATCAGA 1948		
Db 121	AGAAGAAATGCTTCCAAAACCGCAAGTAGACTGGTTATCCACCCACAACATCAGA 180		
QY 1949	ATCGTACTCTCTTAATGATCTAATTTACATATTCGCGTGTGTTATTCAGCAGCTAAAA 2008		
Db 181	ATCGTACTCTCTTAATGATCTAATTTACATATTCGCGTGTGTTATTCAGCAGCTAAAA 240		
QY 2009	ATGGTGGAGCTGGGGAGAGATGAAGACTGTTAATGAACCAAGAGATATTTACTACT 2068		
Db 241	ATGGTGGAGCTGGGGAGAGATGAAGACTGTTAATGAACCAAGAGATATTTACTACT 300		
QY 2069	TTTGATGAAATAGAGCTTCAAGTACATGCTAGCTTTTATGCGAGTCTCTGTTGATG 2128		
Db 301	TTTGATGAAATAGAGCTTCAAGTACATGCTAGCTTTTATGCGAGTCTCTGTTGATG 360		
JY 2129	TTCAATGGGAACCTGGTCAACATGAACTTTAGAGATTAAACGACAAAGATTTTCTACTTTT 2188		
Db 361	TTCAATGGGAACCTGGTCAACATGAACTTTAGAGATTAAACGACAAAGATTTTCTACTTTT 420		
QY 2189	TTAAGTCAATTTTGTCTTCAGCAACACAAATATGGGCTCAGCTCACTTTATTTGAA 2248		
Db 421	NNNNNNNNNNNGTCTTCAGCAACACAAATATGGGCTCAGCTCACTTTATTTGAA 480		
QY 2249	ATGTCATTTGGTGGCAGTATTTTAACTGCAATAATAGCTTAACATGATTATTTGAACCT 2308		
Db 481	ATGTCATTTGGTGGCAGTATTTTAACTGCAATAATAGCTTAACATGATTATTTGAACCT 540		
QY 2309	ATTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTTTACAGTGAGCAATTAGATTA 2368		
Db 541	ATTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTTTACAGTGAGCAATTAGATTA 600		
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Db 601	GTATTTCCAGTCACATTTATTTTAAACACAAATTTTAAAGCTACAAATAAC 660		
QY 2429	TACAGGCCCTTAAGCAGCTGATGACACATTTGGCAGTTTAAATAGATGTTACTCAA 2488		
Db 661	TACAGGCCCTTAAGCAGCTGATGACACATTTGGCAGTTTAAATAGATGTTACTCAA 720		
QY 2489	GAATTTTAAAGAACTGATTTTATTTTAAATGGTGTGTTTATTAACAGGACCTTCAA 2548		

Db 721	GAATTTTAAAGAACTGATATTTTATTTTAAATGGTGTGTTTATTAACAAGGGACCTTGAA 780	
QY 2549	CATGTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTCTTTTTCACAAGT 2608	
Db 781	CATGTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTCTTTTTCACAAGT 840	
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Db 841	TCAATACATGTTTTCATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 900	
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Db 1621	TGTAATCATGTTTACCATTTACAAATGGATATAGAGGCGAGCTGAAAGCAGATGAGCTGT 1680	
QY 3449	GGACTAGCAATATAGGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3508	
Db 1681	GGACTAGCAATATAGGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1740	
QY 3509	TATTTGTTTCTGCTGGGCAAAAGTCAATTCATCTTCAAGTATTTATTTCTTCTTATC 3568	
Db 1741	TATTTGTTTCTGCTGGGCAAAAGTCAATTCATCTTCAAGTATTTATTTCTTCTTATC 1800	
QY 3569	CTCAATCAATGCTGTGATGAAATTTGCCAGGTGCTGTATTTCTTCTCAGACTTCGCCA 3628	
Db 1801	CTCAATCAATGCTGTGATGAAATTTGCCAGGTGCTGTATTTCTTCTCAGACTTCGCCA 1860	

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QY 3629 GACAGATTGCTGATAATAAATAGGTAAGATAATTTGTTGGGCCATATTTTAGCAGAGT 3688
Db 1861 GACAGATTGCTGATAATAAATAGGTAAGATAATTTGTTGGGCCATATTTTAGCAGAGT 1920
QY 3689 AAAATAACATCAGGTTCCAGTTGCTTGAATTCGAAGCTTAAGAGTACTGCCCTTTTGTG 3748
Db 1921 AAAATAACATCAGGTTCCAGTTGCTTGAATTCGAAGCTTAAGAGTACTGCCCTTTTGTG 1980
QY 3749 TGTAGCAGTCAAAATCTATTATTCCTACTGGCGCATCATATGCAAGTATATGCGCTATAA 3808
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Db 2161 GTCACAGTGCATTTTATTATGAGCTGCTGTAAGTAACTGTGTTTACTAGCAGGAATATTT 2220
QY 3989 CCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACCTTTGTAGAAATGAGCCAGAAGC 4048
Db 2221 CCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACCTTTGTAGAAATGAGCCAGAAGC 2280
QY 4049 CAAGCCCTGAGTGGCAGTGGCCCATAGTGTAAATTAATAAAGTTTACAGAAACCTT 4105
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RESULT 11
S63938
LOCUS S63938 1868 bp mRNA linear PRI 07-MAY-1993
DEFINITION A-type endothelin receptor [human, placenta, mRNA, 1868 nt].
ACCESSION S63938
VERSION S63938.1 GI:238635
KEYWORDS
SOURCE Homo sapiens placenta.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ADACHI, M., YANG, Y. Y., FURUICHI, Y. and MIYAMOTO, C.
Cloning and characterization of cDNA encoding human A-type
endothelin receptor
Biochem. Biophys. Res. Commun. 180 (3), 1265-1272 (1991)
JOURNAL 92062153
EDLINE 1719979
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 63938] from the original Journal article.
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QY 841 ACCCAGCTCTGGCTTGGAGACCTTATCTATCTGTTGGTTCATTGATCTCCCTATCAATGATT 900
Db 430 ACCCAGCTCTGGCTTGGAGACCTTATCTATCTGTTGGTTCATTGATCTCCCTATCAATGATT 489
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QY 961 GCTGTTCCTCTTTTGGCAGAACTCTCTGGTGGGATCACCGTCTCAACCTCTGCGCTCT 1020
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QY	1861	CTTCTCTCTTAATCACTCCACCAACCAAGAAATGCTTTCCAAACCGCAA-GGTAG	1919
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VERSION			
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			

REFERENCE	Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 3216)		
TITLE	Arai,H., Hori,S., Aramori,I., Ohkubo,H. and Nakanishi,S.		
JOURNAL	Cloning and expression of a cDNA encoding an endothelin receptor		
MEDLINE	Nature 348 (6303), 730-732 (1990)		
PUBMED	91080923		
FEATURES	2175396		
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QY	68	GAGACAGACTGGAGCGGTGTTCTCCGAGATTTTCTTTTCGTCGCGAGACCTCGCGCGC	127
Db	64	GAGCACAGCGGAGCGCGTCTCTCGAGCTTTCTTTTCTTGAGAACCTCTCGCGCGC	123
QY	128	CGGTACAGTATCCCGCTGCTGACGATTTGGAGAGCGGTGGAGAGGCTTCCATCCAT	187
Db	124	CGGCACAGCAGCGCTTTGGTCTGGAGATTCGGACCAAGAGTGGAGAGGCTCCATCC--	181
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QY	248	CCAGAGATTTTCTGAAGCGGGGAAAGCTGTGCAAGCGGAGAGCCCGCGCGCGGAGCC	307
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QY	308	CGGACACCGCGCACCTCCGCGCCACCCACCTTCGCTTTCTCGGCTTCTCTGGGCCA	367
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QY	368	GGCGCGC--CGCGGACCGCGAGCTGTCTGCGACGCGGAGCTCCACGCTGAAAAA	425
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Qy	662	CCCAGCAATGGCTCAATGCAACAATATTTGCCACAGACACTAAAATTACTTTCAGCTTTC	721
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Qy	902	AAGCTGCTGGCTGGGCGCTTGGCTTTTGTATCACAATGACTTTGGGGTATTTCTTTTGGCAAG	961
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Qy	1202	ATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAGATGTAAAGGACTGTGGCTC	1261
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Qy	1262	TTCGGGTTCTATTTCTGTATGGCTTGGTGTGCACCTCGATCTCTTACACCCCTCATGACT	1321
Db	1245	TTCGGGTTCTATTTCTGTATGGCTTGGTGTGCACCTCGATCTTTTACACCCCTCATGACT	1304
Qy	1322	TGTGAGATGTTGAACGAAGGAATGGCAGCTTTGAGAATTTGCCCTCAGTGAACATCTTTAAG	1381
Db	1305	TGTGAGATGTTAAACCCGAAGGAAGGACGCCCTTGAGAAATTTGCCCTCAGTGAACATCTTTAAG	1364
Qy	1382	CAGCGTCGAAGGTGCAAAAACAGTTTTCGCTTGGTGTAAATTTTGGTCTTTGGCTGG	1441
Db	1365	CAGCGTCGAAGGTGCAAAAACAGTTTTCGCTTGGTGTAAATTTTGGTCTTTGGCTGG	1424
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Qy	1502	CGATGTGAATTTACTTGTCTTGTCTGTCTCATGGAATACATCGGTATTAACCTTGGCAACC	1561
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QY	1742	AGCAGCCATAAAGACAGCATGAATCACCACACCCTTAGAAGCACTCTCTGCGTACTCCCATA	1801
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QY	1922	TGGTTTATCCACCCCAACATCTACGAATCGTACTTCTTTAATTTGATCTAAATTTACATAT	1981
Db	1898	ACTGGTTATACCCACAAATTCACAGNATCTTACGTCTTTTGATTTATCTGATTTACTAT	1957
QY	1982	TCCTGCTGTGTATTACGACACTAAAAAATGGTGGAGCTGG--GGCAGAATGAAGACTGT	2039
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Db	2018	TCAGTTAAACACAGAGGATATTTACCACCTTTCCGTGAAAAATAGATTTTTCGAGTACAT	2077
QY	2099	GGCTAGCTTTTATGCGCTTCCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAACATTT	2158
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QY	2638	TGAAAAATCATGTCAGTACCAAAAATGTTAATGTATGTGTCAATTTTAACTCTGCTGAGA	2697
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VERSION			
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AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 1661)	
JOURNAL		Cyr,C., Huebner,K., Druck,T. and Kris,R.	
MEDLINE		Cloning and chromosomal localization of a human endothelin ETA	
PUBMED		receptor	
REMARK		Biochem. Biophys. Res. Commun. 181 (1), 184-190 (1991)	
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Db	73	AAAAAGTGAAGGTGTA	AAAGCACAAGTGC	AAATTAAGAGATATTTCTCTCAAA	TTTGCC	132			
Qy	480	TCAAGATGGA	AAACCTTTGGCTC	AGGCGATCCTTTTGGCTGGC	ACTGGTGGATGTGTAA	539			
Db	133	TCAAGATGGA	AAACCTTTGGCTC	AGGCGATCCTTTTGGCTGGC	ACTGGTGGATGTGTAA	192			
Qy	540	TCAGTGA	TAATCC	TGAGAGATACAGCA	CAATCTAAAGCAATCATGTGATGATTTCACCA	599			
Db	193	TCAGTGA	TAATCC	TGAGAGATACAGCA	CAATCTAAAGCAATCATGTGATGATTTCACCA	252			
Qy	600	CTTTTCTGG	CACAGAGCTC	AGCTTCTCTGGT	TACCACTCATCAACCCCACTAA	TTGGTCC	659		
Db	253	CTTTTCTGG	CACAGAGCTC	AGCTTCTCTGGT	TACCACTCATCAACCCCACTAA	TTGGTCC	312		
Qy	660	TACCAGCA	ATGGCTCA	ATGCACA	AACTATATGCCACACAGCAGACTAA	ATTAATTA	719		
Db	313	TACCCAGCA	ATGGCTCA	ATGCACA	AACTATATGCCACACAGCAGACTAA	ATTAATTA	372		
Qy	720	TCAAATAC	ATTAAACATGTG	ATATCTTGTA	CTATTTTCATCGTCGGGAATGGTGGGGAATG	779			
Db	373	TCAAATAC	ATTAAACATGTG	ATATCTTGTA	CTATTTTCATCGTCGGGAATGGTGGGGAATG	432			
Qy	780	CAACTCTG	CTCAGGATCATTTACC	AGAACAAATGTATGAGGAATGGCCCCAACCGCGTGA	839				
Db	433	CAACTCTG	CTCAGGATCATTTACC	AGAACAAATGTATGAGGAATGGCCCCAACCGCGTGA	492				
Qy	840	TAGCAGTCTT	GGCCCTGGAGAC	CTTATCTATGTGGTCA	TTCATCCCTATCAATGTAT	899			
Db	493	TAGCAGTCTT	GGCCCTGGAGAC	CTTATCTATGTGGTCA	TTCATCCCTATCAATGTAT	552			
Qy	900	TTAAGTCTG	CTGGCTGGCGCTT	TTTGATACAAATGACTTTTGGCGTATTTCTTTGCA	959				
Db	553	TTAAGTCTG	CTGGCTGGCGCTT	TTTGATACAAATGACTTTTGGCGTATTTCTTTGCA	612				
Qy	960	AGCTGTT	CCCCCTTTTG	CAGAAGTCCCTGGTGGGGATCACCGCTCCTCAACCTCTGC	CGCTC 1019				
Db	613	AGCTGTT	CCCCCTTTTG	CAGAAGTCCCTGGTGGGGATCACCGCTCCTCAACCTCTGC	CGCTC 672				
Qy	1020	TAGTGT	TGACAGTACAGAC	AGCATTGGCTCCTGGAGTCGTGTT	CAGGGAATTCGGGATTC 1079				
Db	673	TAGTGT	TGACAGTACAGAC	AGCATTGGCTCCTGGAGTCGTGTT	CAGGGAATTCGGGATTC 732				
Qy	1080	CTTTGGT	TAAC	TGCAATGAAATTGCTCCATCTGGATCCTCTCCTTTATCTCGTGGCCATTC	1139				
Db	733	CTTTGGT	TAAC	TGCAATGAAATTGCTCCATCTGGATCCTCTCCTTTATCTCGTGGCCATTC	792				
Qy	1140	CTGAAGC	GATTGGCTTC	GTTCATGTGATACCCCTTTGAATATAGGGGTGAACAGCATAAAAACCT	1199				
Db	793	CTGAAGC	GATTGGCTTC	GTTCATGTGATACCCCTTTGAATATAGGGGTGAACAGCATAAAAACCT	852				
Qy	1200	GTATGCT	CAATGCCACATCAAAATTC	ATGGAGTCTTACCAAGATGTAAAGACTGTGGTGC	1259				
Db	853	GTATGCT	CAATGCCACATCAAAATTC	ATGGAGTCTTACCAAGATGTAAAGACTGTGGTGC	912				

QY	1260	TCTTCGGGTTCTATTCTGTATGCCCTTGGTGTGCACCTGCCATCTTCTACACCCCTCATGA	1319
Db	913	TCTTCGGGTTCTATTCTGTATGCCCTTGGTGTGCACCTGCCATCTTCTACACCCCTCATGA	972
QY	1320	CTTGTGAGATGTTGAACAGAAGGATGCGACCTTCAGAAATTCGCCCTCAGTGAACATCTTA	1379
Db	973	CTTGTGAGATGTTGNACAGAAGGATGCGACCTTCAGAAATTCGCCCTCAGTGAACATCTTA	1032
QY	1380	AGCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTGGTGTGTAATTTTCTGCTCTTTGCT	1439
Db	1033	AGCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTGGTGTGTAATTTTCTGCTCTTTGCT	1092
QY	1440	GGTTCCCTCTTCACCTTAAGCCGTATATTGAAGAAACACTGTGTATAGCAAAATGGACAAGA	1499
Db	1093	GGTTCCCTCTTCATTTAAGCCGTATATTGAAGAAACACTGTGTATAGCAAAATGGACAAGA	1152
QY	1500	ACCGATGTGAATTAATTAATTTCTACTGCTCATGGATATACATCGGTATTAACCTTGCGAA	1559
Db	1153	ACCGATGTGAATTAATTTCTACTGCTCATGGATATACATCGGTATTAACCTTGCGAA	1212
QY	1560	CCATGAATTCATGATATAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATT	1619
Db	1213	CCATGAATTCATGATATAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATT	1272
QY	1620	GTTTCCAGTCATGCTCTGCTGCTGTGTACCAGTCCAAAAGTCTGATGACCTCGGTCC	1679
Db	1273	GTTTCCAGTCATGCTCTGCTGCTGTGTACCAGTCCAAAAGTCTGATGACCTCGGTCC	1332
QY	1680	CCATGAACGGAACAGCATCCAGTGGAGAACACACGATCAAAACACCAACACAGACC	1739
Db	1333	CCATGAACGGAACAGCATCCAGTGGAGAACACACGATCAAAACACCAACACAGACC	1392
QY	1740	GGAGCAGCCATAAGGACAGCATGAACCTGACACACCCCTTAGAAGCACTCTCGGTACTCCCA	1799
Db	1393	GGAGCAGCCATAAGGACAGCATGAACCTGACACACCCCTTAGAAGCACTCTCGGTACTCCCA	1452
QY	1800	TAATCCTCTCGGAGAAAAAATCAACAGGCACTGTGACCTCCGGGAATCTTCTCTGAT	1859
Db	1453	TAATCCTCTCGGAGAAAAAATCAACAGGCACTGTGACCTCCGGGAATCTTCTCTGAT	1512
QY	1860	CTTCTCTCTTAATTAATCTCCACACCCCAAGAAATGCTTTCCAAACCCGCAAGTAG	1919
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QY	1920	ACTGGTTATCCACCCACACATCTACGAATCGTACTTC-TTTAATGTACTTAATTTACA	1978
Db	1573	ACTGGTTATCCACCCACACATCTACGAATCGTACTTC-TTTAATGTACTTAATTTACA	1632
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RESULT	14		
LOCUS	S81539	1359 bp	linear
DEFINITION	endothelin-A receptor-ET-AR [human, lung, mRNA	PRI 03-AUG-1996	
ACCESSION	S81539		
VERSION	S81539.1	GI:1478475	
KEYWORDS	Homo sapiens lung.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1359)		
AUTHORS	Miyamoto, Y., Yoshimasa, T., Arai, H., Takaya, K., Ogawa, Y., Itoh, H. and Nakao, K.		
TITLE	Alternative RNA splicing of the human endothelin-A receptor generates multiple transcripts		
JOURNAL	Biochem. J. 313 (Pt 3), 795-801 (1996)		
MEDLINE	96190719		
PUBMED	8611157		

Db	601	GTAACGCCATGAAATGTCTCCACTGTGGATCTCTCTTTATCTCTGCCATCTCTGAA	660
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Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
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Qy	1265	GGTTCCTATTCTGTATGCCCTTGGTGTGCATCGATCGATCTTCTACACCTCATGACTTGT	1324
Db	781	GGTTCCTATTCTGTATGCCCTTGGTGTGCATCGATCGATCTTCTACACCTCATGACTTGT	840
Qy	1325	GAGATGTTGAACAGCAAGATGGCAGCTTGAGATTCGCCCTCAGTGAACATCTTAAGCAG	1384
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Qy	1445	CTCTTTCACCTTAAGCCGTATATTGAAGAAACTGTGTATACGAAATGGCAAGAACCGA	1504
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Qy	1505	TGTGAATTACTTACTTCTTACTGCTCATGGATTCATCGGTATTAATCTGGCAACCATG	1564
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Qy	1565	AATTCATGTATAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTTAAATTTGTTTC	1624
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Qy	1625	CAGTCATGCTCTGCTGCTGTGTACAGTCCAAAGTCTGTAGTACCTCGTCCCATG	1684
Db	1141	CAGTCATGCTCTGCTGCTGTGTACAGTCCAAAGTCTGTAGTACCTCGTCCCATG	1200
Qy	1685	AACGGACACAGCATCCAGTGGAGAACCCAGATCAAAACACACACAGACCGGAGC	1744
Db	1201	AACGGACACAGCATCCAGTGGAGAACCCAGATCAAAACACACACAGACCGGAGC	1260
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RESULT 15			
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DEFINITION Homo sapiens endothelin receptor type A (EDNRA) mRNA, complete cds.			
ACCESSION L06622.1			
VERSION 1 (bases 1 to 1310)			
KEYWORDS endothelin receptor; endothelin receptor type A.			
SOURCE Homo sapiens (tissue library: lambda ZAPII) heart, left ventricle			
CDNA to mRNA.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1 (bases 1 to 1310)			
AUTHORS Elshourbagy, N.A., Korman, D.R., Wu, H.L., Sylvester, D.R., Lee, J.A., Nuthallagan, P., Bergsma, D.J., Kumar, C.S. and Nambip, P.			
TITLE Molecular characterization and regulation of the human endothelin receptors			
JOURNAL J. Biol. Chem. 268 (6), 3873-3879 (1993)			
MEDLINE 93179382			
PUBMED 8440682			
FEATURES			
Location/Qualifiers			
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BASE COUNT 337 a 312 c 284 g 377 t			
ORIGIN			
Query Match 31.6%; Score 1296.8; DB 9; Length 1310;			
Best Local Similarity 99.5%; Pred. No. 2.9e-282;			
Matches 1301; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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Db	3	CACCATGGAACCCCTTGGCTCAGGGCATCTTTGGCTGGCACTGTTGGGATGTGTAAT	62
Qy	541	CAGTGATTAATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTTACCAC	600
Db	63	CAGTGATTAATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTTACCAC	122
Qy	601	TTTTCGTGGCAGAGCTCAGCTTCTGTTTACCACTCATCAACCCACATAATTTGGTCTCT	660
Db	123	TTTTCGTGGCAGAGCTCAGCTTCTGTTTACCACTCATCAACCCACATAATTTGGTCTCT	182
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAATTTACTTCACTTT	720
Db	183	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAATTTACTTCACTTT	242
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Db	243	CAATACATTAACACTGTGATATCTTGACTATTTTATCTGTTGGGAAATGGTGGGAAATGC	302
Qy	781	AACCTCTCTCAGGATCATTTACCAACAATAATGTAGGAATGGCCCAACGCGCTGAT	840
Db	303	AACCTCTCTCAGGATCATTTACCAACAATAATGTAGGAATGGCCCAACGCGCTGAT	362
Qy	841	AGCCAGTCTTGGCTTGGAGACTTTATCTATGTTGGTCTATCTCCCTATCAATGATTT	900
Db	363	AGCCAGTCTTGGCTTGGAGACTTTATCTATGTTGGTCTATCTCCCTATCAATGATTT	422
Qy	901	TAAGTCTGCTGGCTGGGCTGGCCCTTTTATCACAATGACTTTGGCGTATTTCTTTTGCAA	960
Db	423	TAAGTCTGCTGGCTGGGCTGGCCCTTTTATCACAATGACTTTGGCGTATTTCTTTTGCAA	482
Qy	961	GCTGTTCCCTTTTTCAGAGAAGTCTCTCGTGGGGATCACCGTCTCAACCTCTGCGCTCT	1020
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Qy	1021	TAGTCTTTCAGAGTACAGAGAGTTCCTCTCGAGTCTGTTTCAGGAAATGGGATTC	1080
Db	543	TAGTCTTTCAGAGTACAGAGAGTTCCTCTCGAGTCTGTTTCAGGAAATGGGATTC	602
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Db	603	TTTGTAATGCCATTAATTTGCTCCATCTCGATCTCTGCTCTTATCTTCCCTGATTC	662
Qy	1141	TGAAGCGATTCGCTCGTACCGCTTTTGAATATAGGGGTGAACAGCATAAACCTG	1200

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